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(54) Title: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

(57) Abstract: The present invention is directed to novel polypeptides and to nucleic acid molecules encoding those polypeptides. Also provided herein are vectors and host cells comprising those nucleic acid sequences, chimeric polypeptide molecules comprising the polypeptides of the present invention fused to heterologous polypeptide sequences, antibodies which bind to the polypeptides of the present invention and to methods for producing the polypeptides of the present invention.

# SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME

## FIELD OF THE INVENTION

The present invention relates generally to the identification and isolation of novel DNA and to the recombinant production of novel polypeptides.

## BACKGROUND OF THE INVENTION

Extracellular proteins play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. These secreted polypeptides or signaling molecules normally pass through the cellular secretory pathway to reach their site of action in the extracellular environment.

Secreted proteins have various industrial applications, including as pharmaceuticals, diagnostics, biosensors and bioreactors. Most protein drugs available at present, such as thrombolytic agents, interferons, interleukins, erythropoietins, colony stimulating factors, and various other cytokines, are secretory proteins. Their receptors, which are membrane proteins, also have potential as therapeutic or diagnostic agents. Efforts are being undertaken by both industry and academia to identify new, native secreted proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel secreted proteins. Examples of screening methods and techniques are described in the literature [see, for example, Klein et al., Proc. Natl. Acad. Sci. 93:7108-7113 (1996); U.S. Patent No. 5,536,637)].

Membrane-bound proteins and receptors can play important roles in, among other things, the formation, differentiation and maintenance of multicellular organisms. The fate of many individual cells, e.g., proliferation, migration, differentiation, or interaction with other cells, is typically governed by information received from other cells and/or the immediate environment. This information is often transmitted by secreted polypeptides (for instance, mitogenic factors, survival factors, cytotoxic factors, differentiation factors, neuropeptides, and hormones) which are, in turn, received and interpreted by diverse cell receptors or membrane-bound proteins. Such membrane-bound proteins and cell receptors include, but are not limited to, cytokine receptors, receptor kinases, receptor phosphatases, receptors involved in cell-cell interactions, and cellular adhesin molecules like selectins and integrins. For instance, transduction of signals that regulate cell growth and differentiation is regulated in part by phosphorylation of various cellular proteins. Protein tyrosine kinases, enzymes that catalyze that process, can also act as growth factor receptors. Examples include fibroblast growth factor receptor and

nerve growth factor receptor.

Membrane-bound proteins and receptor molecules have various industrial applications, including as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be employed as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction.

Efforts are being undertaken by both industry and academia to identify new, native receptor or membrane-bound proteins. Many efforts are focused on the screening of mammalian recombinant DNA libraries to identify the coding sequences for novel receptor or membrane-bound proteins.

## SUMMARY OF THE INVENTION

In one embodiment, the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence that encodes a PRO polypeptide.

In one aspect, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule encoding a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In other aspects, the isolated nucleic acid molecule comprises a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94%

nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule comprising the coding sequence of a full-length PRO polypeptide cDNA as disclosed herein, the coding sequence of a PRO polypeptide lacking the signal peptide as disclosed herein, the coding sequence of an extracellular domain of a transmembrane PRO polypeptide, with or without the signal peptide, as disclosed herein or the coding sequence of any other specifically defined fragment of the full-length amino acid sequence as disclosed herein, or (b) the complement of the DNA molecule of (a).

In a further aspect, the invention concerns an isolated nucleic acid molecule comprising a nucleotide sequence having at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity to (a) a DNA molecule that encodes the same mature polypeptide encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein, or (b) the complement of the DNA molecule of (a).

Another aspect the invention provides an isolated nucleic acid molecule comprising a nucleotide sequence encoding a PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated, or is complementary to such encoding nucleotide sequence, wherein the transmembrane domain(s) of such polypeptide are disclosed herein. Therefore, soluble extracellular domains of the herein described PRO polypeptides are contemplated.

Another embodiment is directed to fragments of a PRO polypeptide coding sequence, or the complement thereof, that may find use as, for example, hybridization probes, for encoding fragments of a PRO polypeptide that may optionally encode a polypeptide comprising a binding site for an anti-PRO antibody or as antisense oligonucleotide probes. Such nucleic acid fragments are usually at least about 10 nucleotides in length, alternatively at least about 15 nucleotides in length, alternatively at least about 20 nucleotides in length, alternatively at least about 30 nucleotides in length, alternatively at least about 40 nucleotides in length, alternatively at least about 50 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 70 nucleotides in length, alternatively at least about 80 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 100 nucleotides in length, alternatively at least about 110 nucleotides in length, alternatively at least about 120 nucleotides in length,

alternatively at least about 130 nucleotides in length, alternatively at least about 140 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 160 nucleotides in length, alternatively at least about 170 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 190 nucleotides in length, alternatively at least about 200 nucleotides in length, alternatively at least about 250 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 350 nucleotides in length, alternatively at least about 400 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 500 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 700 nucleotides in length, alternatively at least about 800 nucleotides in length, alternatively at least about 900 nucleotides in length and alternatively at least about 1000 nucleotides in length, wherein in this context the term "about" means the referenced nucleotide sequence length plus or minus 10% of that referenced length. It is noted that novel fragments of a PRO polypeptide-encoding nucleotide sequence may be determined in a routine manner by aligning the PRO polypeptide-encoding nucleotide sequence with other known nucleotide sequences using any of a number of well known sequence alignment programs and determining which PRO polypeptide-encoding nucleotide sequence fragment(s) are novel. All of such PRO polypeptide-encoding nucleotide sequences are contemplated herein. Also contemplated are the PRO polypeptide fragments encoded by these nucleotide molecule fragments, preferably those PRO polypeptide fragments that comprise a binding site for an anti-PRO antibody.

In another embodiment, the invention provides isolated PRO polypeptide encoded by any of the isolated nucleic acid sequences hereinabove identified.

In a certain aspect, the invention concerns an isolated PRO polypeptide, comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a PRO polypeptide having a full-length amino acid sequence as disclosed herein, an amino acid sequence lacking the signal peptide as disclosed herein, an extracellular domain of a transmembrane protein, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of the full-length amino acid sequence as disclosed herein.

In a further aspect, the invention concerns an isolated PRO polypeptide comprising an amino acid sequence having at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83%

amino acid sequence identity, alternatively at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to an amino acid sequence encoded by any of the human protein cDNAs deposited with the ATCC as disclosed herein.

In a specific aspect, the invention provides an isolated PRO polypeptide without the N-terminal signal sequence and/or the initiating methionine and is encoded by a nucleotide sequence that encodes such an amino acid sequence as hereinbefore described. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

Another aspect the invention provides an isolated PRO polypeptide which is either transmembrane domain-deleted or transmembrane domain-inactivated. Processes for producing the same are also herein described, wherein those processes comprise culturing a host cell comprising a vector which comprises the appropriate encoding nucleic acid molecule under conditions suitable for expression of the PRO polypeptide and recovering the PRO polypeptide from the cell culture.

In yet another embodiment, the invention concerns agonists and antagonists of a native PRO polypeptide as defined herein. In a particular embodiment, the agonist or antagonist is an anti-PRO antibody or a small molecule.

In a further embodiment, the invention concerns a method of identifying agonists or antagonists to a PRO polypeptide which comprise contacting the PRO polypeptide with a candidate molecule and monitoring a biological activity mediated by said PRO polypeptide. Preferably, the PRO polypeptide is a native PRO polypeptide.

In a still further embodiment, the invention concerns a composition of matter comprising a PRO polypeptide, or an agonist or antagonist of a PRO polypeptide as herein described, or an anti-PRO antibody, in combination with a carrier. Optionally, the carrier is a pharmaceutically acceptable carrier.

Another embodiment of the present invention is directed to the use of a PRO polypeptide, or an agonist or antagonist thereof as hereinbefore described, or an anti-PRO antibody, for the preparation of a medicament useful in the treatment of a condition which is responsive to the PRO polypeptide, an agonist or antagonist thereof or an anti-PRO antibody.

In other embodiments of the present invention, the invention provides vectors comprising DNA encoding any of the herein described polypeptides. Host cell comprising any such vector are also provided. By way of example, the host cells may be CHO cells, *E. coli*, or yeast. A process for producing any of the herein described

polypeptides is further provided and comprises culturing host cells under conditions suitable for expression of the desired polypeptide and recovering the desired polypeptide from the cell culture.

In other embodiments, the invention provides chimeric molecules comprising any of the herein described polypeptides fused to a heterologous polypeptide or amino acid sequence. Example of such chimeric molecules comprise any of the herein described polypeptides fused to an epitope tag sequence or a Fc region of an immunoglobulin.

In another embodiment, the invention provides an antibody which binds, preferably specifically, to any of the above or below described polypeptides. Optionally, the antibody is a monoclonal antibody, humanized antibody, antibody fragment or single-chain antibody.

In yet other embodiments, the invention provides oligonucleotide probes which may be useful for isolating genomic and cDNA nucleotide sequences, measuring or detecting expression of an associated gene or as antisense probes, wherein those probes may be derived from any of the above or below described nucleotide sequences. Preferred probe lengths are described above.

In yet other embodiments, the present invention is directed to methods of using the PRO polypeptides of the present invention for a variety of uses based upon the functional biological assay data presented in the Examples below.

## BRIEF DESCRIPTION OF THE DRAWINGS

Figure 1 shows a nucleotide sequence (SEQ ID NO:1) of a native sequence PRO281 cDNA, wherein SEQ ID NO:1 is a clone designated herein as "DNA16422-1209".

Figure 2 shows the amino acid sequence (SEQ ID NO:2) derived from the coding sequence of SEQ ID NO:1 shown in Figure 1.

Figure 3 shows a nucleotide sequence (SEQ ID NO:3) of a native sequence PRO1560 cDNA, wherein SEQ ID NO:3 is a clone designated herein as "DNA19902-1669".

Figure 4 shows the amino acid sequence (SEQ ID NO:4) derived from the coding sequence of SEQ ID NO:3 shown in Figure 3.

Figure 5 shows a nucleotide sequence (SEQ ID NO:5) of a native sequence PRO189 cDNA, wherein SEQ ID NO:5 is a clone designated herein as "DNA21624-1391".

Figure 6 shows the amino acid sequence (SEQ ID NO:6) derived from the coding sequence of SEQ ID NO:5 shown in Figure 5.

Figure 7 shows a nucleotide sequence (SEQ ID NO:7) of a native sequence PRO240 cDNA, wherein SEQ ID NO:7 is a clone designated herein as "DNA34387-1138".

Figure 8 shows the amino acid sequence (SEQ ID NO:8) derived from the coding sequence of SEQ ID NO:7 shown in Figure 7.

Figure 9 shows a nucleotide sequence (SEQ ID NO:9) of a native sequence PRO256 cDNA, wherein SEQ ID NO:9 is a clone designated herein as "DNA35880-1160".

Figure 10 shows the amino acid sequence (SEQ ID NO:10) derived from the coding sequence of SEQ ID NO:9 shown in Figure 9.

Figure 11 shows a nucleotide sequence (SEQ ID NO:11) of a native sequence PRO306 cDNA, wherein SEQ ID NO:11 is a clone designated herein as "DNA39984-1221".

Figure 12 shows the amino acid sequence (SEQ ID NO:12) derived from the coding sequence of SEQ ID NO:11 shown in Figure 11.

Figure 13 shows a nucleotide sequence (SEQ ID NO:13) of a native sequence PRO540 cDNA, wherein SEQ ID NO:13 is a clone designated herein as "DNA44189-1322".

Figure 14 shows the amino acid sequence (SEQ ID NO:14) derived from the coding sequence of SEQ ID NO:13 shown in Figure 13.

Figure 15 shows a nucleotide sequence (SEQ ID NO:15) of a native sequence PRO773 cDNA, wherein SEQ ID NO:15 is a clone designated herein as "DNA48303-2829".

Figure 16 shows the amino acid sequence (SEQ ID NO:16) derived from the coding sequence of SEQ ID NO:15 shown in Figure 15.

Figure 17 shows a nucleotide sequence (SEQ ID NO:17) of a native sequence PRO698 cDNA, wherein SEQ ID NO:17 is a clone designated herein as "DNA48320-1433".

Figure 18 shows the amino acid sequence (SEQ ID NO:18) derived from the coding sequence of SEQ ID NO:17 shown in Figure 17.

Figure 19 shows a nucleotide sequence (SEQ ID NO:19) of a native sequence PRO3567 cDNA, wherein SEQ ID NO:19 is a clone designated herein as "DNA56049-2543".

Figure 20 shows the amino acid sequence (SEQ ID NO:20) derived from the coding sequence of SEQ ID NO:19 shown in Figure 19.

Figure 21 shows a nucleotide sequence (SEQ ID NO:21) of a native sequence PRO826 cDNA, wherein SEQ ID NO:21 is a clone designated herein as "DNA57694-1341".

Figure 22 shows the amino acid sequence (SEQ ID NO:22) derived from the coding sequence of SEQ ID NO:21 shown in Figure 21.

Figure 23 shows a nucleotide sequence (SEQ ID NO:23) of a native sequence PRO1002 cDNA, wherein SEQ ID NO:23 is a clone designated herein as "DNA59208-1373".

Figure 24 shows the amino acid sequence (SEQ ID NO:24) derived from the coding sequence of SEQ ID NO:23 shown in Figure 23.

Figure 25 shows a nucleotide sequence (SEQ ID NO:25) of a native sequence PRO1068 cDNA, wherein SEQ ID NO:25 is a clone designated herein as "DNA59214-1449".

Figure 26 shows the amino acid sequence (SEQ ID NO:26) derived from the coding sequence of SEQ ID NO:25 shown in Figure 25.

Figure 27 shows a nucleotide sequence (SEQ ID NO:27) of a native sequence PRO1030 cDNA, wherein SEQ ID NO:27 is a clone designated herein as "DNA59485-1336".

Figure 28 shows the amino acid sequence (SEQ ID NO:28) derived from the coding sequence of SEQ ID NO:27 shown in Figure 27.

Figure 29 shows a nucleotide sequence (SEQ ID NO:29) of a native sequence PRO1313 cDNA, wherein SEQ ID NO:29 is a clone designated herein as "DNA64966-1575".

Figure 30 shows the amino acid sequence (SEQ ID NO:30) derived from the coding sequence of SEQ ID NO:29 shown in Figure 29.

Figure 31 shows a nucleotide sequence (SEQ ID NO:31) of a native sequence PRO6071 cDNA, wherein SEQ ID NO:31 is a clone designated herein as "DNA82403-2959".

Figure 32 shows the amino acid sequence (SEQ ID NO:32) derived from the coding sequence of SEQ ID NO:31 shown in Figure 31.

Figure 33 shows a nucleotide sequence (SEQ ID NO:33) of a native sequence PRO4397 cDNA, wherein SEQ ID NO:33 is a clone designated herein as "DNA83505-2606".

Figure 34 shows the amino acid sequence (SEQ ID NO:34) derived from the coding sequence of SEQ ID NO:33 shown in Figure 33.

Figure 35 shows a nucleotide sequence (SEQ ID NO:35) of a native sequence PRO4344 cDNA, wherein SEQ ID NO:35 is a clone designated herein as "DNA84927-2585".

Figure 36 shows the amino acid sequence (SEQ ID NO:36) derived from the coding sequence of SEQ ID NO:35 shown in Figure 35.

Figure 37 shows a nucleotide sequence (SEQ ID NO:37) of a native sequence PRO4407 cDNA, wherein SEQ ID NO:37 is a clone designated herein as "DNA92264-2616".

Figure 38 shows the amino acid sequence (SEQ ID NO:38) derived from the coding sequence of SEQ ID NO:37 shown in Figure 37.

Figure 39 shows a nucleotide sequence (SEQ ID NO:39) of a native sequence PRO4316 cDNA, wherein SEQ ID NO:39 is a clone designated herein as "DNA94713-2561".

Figure 40 shows the amino acid sequence (SEQ ID NO:40) derived from the coding sequence of SEQ ID NO:39 shown in Figure 39.

Figure 41 shows a nucleotide sequence (SEQ ID NO:41) of a native sequence PRO5775 cDNA, wherein SEQ ID NO:41 is a clone designated herein as "DNA96869-2673".

Figure 42 shows the amino acid sequence (SEQ ID NO:42) derived from the coding sequence of SEQ ID NO:41 shown in Figure 41.

Figure 43 shows a nucleotide sequence (SEQ ID NO:43) of a native sequence PRO6016 cDNA, wherein SEQ ID NO:43 is a clone designated herein as "DNA96881-2699".

Figure 44 shows the amino acid sequence (SEQ ID NO:44) derived from the coding sequence of SEQ ID NO:43 shown in Figure 43.

Figure 45 shows a nucleotide sequence (SEQ ID NO:45) of a native sequence PRO4499 cDNA, wherein SEQ ID NO:45 is a clone designated herein as "DNA96889-2641".

Figure 46 shows the amino acid sequence (SEQ ID NO:46) derived from the coding sequence of SEQ ID NO:45 shown in Figure 45.

Figure 47 shows a nucleotide sequence (SEQ ID NO:47) of a native sequence PRO4487 cDNA, wherein SEQ ID NO:47 is a clone designated herein as "DNA96898-2640".

Figure 48 shows the amino acid sequence (SEQ ID NO:48) derived from the coding sequence of SEQ ID NO:47 shown in Figure 47.

Figure 49 shows a nucleotide sequence (SEQ ID NO:49) of a native sequence PRO4980 cDNA, wherein SEQ ID NO:49 is a clone designated herein as "DNA97003-2649".

Figure 50 shows the amino acid sequence (SEQ ID NO:50) derived from the coding sequence of SEQ ID NO:49 shown in Figure 49.

Figure 51 shows a nucleotide sequence (SEQ ID NO:51) of a native sequence PRO6018 cDNA, wherein SEQ ID NO:51 is a clone designated herein as "DNA98565-2701".

Figure 52 shows the amino acid sequence (SEQ ID NO:52) derived from the coding sequence of SEQ ID NO:51 shown in Figure 51.

Figure 53 shows a nucleotide sequence (SEQ ID NO:53) of a native sequence PRO7168 cDNA, wherein SEQ ID NO:53 is a clone designated herein as "DNA102846-2742".

Figure 54 shows the amino acid sequence (SEQ ID NO:54) derived from the coding sequence of SEQ ID NO:53 shown in Figure 53.

Figure 55 shows a nucleotide sequence (SEQ ID NO:55) of a native sequence PRO6308 cDNA, wherein SEQ ID NO:55 is a clone designated herein as "DNA102847-2726".

Figure 56 shows the amino acid sequence (SEQ ID NO:56) derived from the coding sequence of SEQ ID NO:55 shown in Figure 55.

Figure 57 shows a nucleotide sequence (SEQ ID NO:57) of a native sequence PRO6000 cDNA, wherein SEQ ID NO:57 is a clone designated herein as "DNA102880-2689".

Figure 58 shows the amino acid sequence (SEQ ID NO:58) derived from the coding sequence of SEQ ID NO:57 shown in Figure 57.

Figure 59 shows a nucleotide sequence (SEQ ID NO:59) of a native sequence PRO6006 cDNA, wherein SEQ ID NO:59 is a clone designated herein as "DNA105782-2693".

Figure 60 shows the amino acid sequence (SEQ ID NO:60) derived from the coding sequence of SEQ ID NO:59 shown in Figure 59.

Figure 61 shows a nucleotide sequence (SEQ ID NO:61) of a native sequence PRO5800 cDNA, wherein SEQ ID NO:61 is a clone designated herein as "DNA108912-2680".

Figure 62 shows the amino acid sequence (SEQ ID NO:62) derived from the coding sequence of SEQ ID NO:61 shown in Figure 61.

Figure 63 shows a nucleotide sequence (SEQ ID NO:63) of a native sequence PRO7476 cDNA, wherein SEQ ID NO:63 is a clone designated herein as "DNA115253-2757".

Figure 64 shows the amino acid sequence (SEQ ID NO:64) derived from the coding sequence of SEQ ID NO:63 shown in Figure 63.

Figure 65 shows a nucleotide sequence (SEQ ID NO:65) of a native sequence PRO6496 cDNA, wherein SEQ ID NO:65 is a clone designated herein as "DNA119302-2737".

Figure 66 shows the amino acid sequence (SEQ ID NO:66) derived from the coding sequence of SEQ ID NO:65 shown in Figure 65.

Figure 67 shows a nucleotide sequence (SEQ ID NO:67) of a native sequence PRO7422 cDNA, wherein SEQ ID NO:67 is a clone designated herein as "DNA119536-2752".

Figure 68 shows the amino acid sequence (SEQ ID NO:68) derived from the coding sequence of SEQ ID NO:67 shown in Figure 67.

Figure 69 shows a nucleotide sequence (SEQ ID NO:69) of a native sequence PRO7431cDNA, wherein SEQ ID NO:69 is a clone designated herein as "DNA119542-2754".

Figure 70 shows the amino acid sequence (SEQ ID NO:70) derived from the coding sequence of SEQ ID NO:69 shown in Figure 69.

Figure 71 shows a nucleotide sequence (SEQ ID NO:71) of a native sequence PRO10275 cDNA, wherein SEQ ID NO:71 is a clone designated herein as "DNA143498-2824".

Figure 72 shows the amino acid sequence (SEQ ID NO:72) derived from the coding sequence of SEQ ID NO:71 shown in Figure 71.

Figure 73 shows a nucleotide sequence (SEQ ID NO:73) of a native sequence PRO10268 cDNA, wherein SEQ ID NO:73 is a clone designated herein as "DNA145583-2820".

Figure 74 shows the amino acid sequence (SEQ ID NO:74) derived from the coding sequence of SEQ ID NO:73 shown in Figure 73.

Figure 75 shows a nucleotide sequence (SEQ ID NO:75) of a native sequence PRO20080 cDNA, wherein SEQ ID NO:75 is a clone designated herein as "DNA161000-2896".

Figure 76 shows the amino acid sequence (SEQ ID NO:76) derived from the coding sequence of SEQ ID NO:75 shown in Figure 75.

Figure 77 shows a nucleotide sequence (SEQ ID NO:77) of a native sequence PRO21207 cDNA, wherein SEQ ID NO:77 is a clone designated herein as "DNA161005-2943".

Figure 78 shows the amino acid sequence (SEQ ID NO:78) derived from the coding sequence of SEQ ID NO:77 shown in Figure 77.

Figure 79 shows a nucleotide sequence (SEQ ID NO:79) of a native sequence PRO28633 cDNA, wherein SEQ ID NO:79 is a clone designated herein as "DNA170245-3053".

Figure 80 shows the amino acid sequence (SEQ ID NO:80) derived from the coding sequence of SEQ ID NO:79 shown in Figure 79.

Figure 81 shows a nucleotide sequence (SEQ ID NO:81) of a native sequence PRO20933 cDNA, wherein SEQ ID NO:81 is a clone designated herein as "DNA171771-2919".

Figure 82 shows the amino acid sequence (SEQ ID NO:82) derived from the coding sequence of SEQ ID NO:81 shown in Figure 81.

Figure 83 shows a nucleotide sequence (SEQ ID NO:83) of a native sequence PRO21383 cDNA, wherein SEQ ID NO:83 is a clone designated herein as "DNA173157-2981".

Figure 84 shows the amino acid sequence (SEQ ID NO:84) derived from the coding sequence of SEQ ID NO:83 shown in Figure 83.

Figure 85 shows a nucleotide sequence (SEQ ID NO:85) of a native sequence PRO21485 cDNA, wherein SEQ ID NO:85 is a clone designated herein as "DNA175734-2985".

Figure 86 shows the amino acid sequence (SEQ ID NO:86) derived from the coding sequence of SEQ ID NO:85 shown in Figure 85.

Figure 87 shows a nucleotide sequence (SEQ ID NO:87) of a native sequence PRO28700 cDNA, wherein SEQ ID NO:87 is a clone designated herein as "DNA176108-3040".

Figure 88 shows the amino acid sequence (SEQ ID NO:88) derived from the coding sequence of SEQ ID NO:87 shown in Figure 87.

Figure 89 shows a nucleotide sequence (SEQ ID NO:89) of a native sequence PRO34012 cDNA, wherein SEQ ID NO:89 is a clone designated herein as "DNA190710-3028".

Figure 90 shows the amino acid sequence (SEQ ID NO:90) derived from the coding sequence of SEQ ID NO:89 shown in Figure 89.

Figure 91 shows a nucleotide sequence (SEQ ID NO:91) of a native sequence PRO34003 cDNA, wherein SEQ ID NO:91 is a clone designated herein as "DNA190803-3019".

Figure 92 shows the amino acid sequence (SEQ ID NO:92) derived from the coding sequence of SEQ ID NO:91 shown in Figure 91.

Figure 93 shows a nucleotide sequence (SEQ ID NO:93) of a native sequence PRO34274 cDNA, wherein SEQ ID NO:93 is a clone designated herein as "DNA191064-3069".

Figure 94 shows the amino acid sequence (SEQ ID NO:94) derived from the coding sequence of SEQ ID NO:93 shown in Figure 93.

Figures 95A-95B shows a nucleotide sequence (SEQ ID NO:95) of a native sequence PRO34001 cDNA, wherein SEQ ID NO:95 is a clone designated herein as "DNA194909-3013".

Figure 96 shows the amino acid sequence (SEQ ID NO:96) derived from the coding sequence of SEQ ID NO:95 shown in Figures 95A-95B.

Figure 97 shows a nucleotide sequence (SEQ ID NO:97) of a native sequence PRO34009 cDNA, wherein SEQ ID NO:97 is a clone designated herein as "DNA203532-3029".

Figure 98 shows the amino acid sequence (SEQ ID NO:98) derived from the coding sequence of SEQ ID NO:97 shown in Figure 97.

Figure 99 shows a nucleotide sequence (SEQ ID NO:99) of a native sequence PRO34192 cDNA, wherein SEQ ID NO:99 is a clone designated herein as "DNA213858-3060".

Figure 100 shows the amino acid sequence (SEQ ID NO:100) derived from the coding sequence of SEQ ID NO:99 shown in Figure 99.

Figure 101 shows a nucleotide sequence (SEQ ID NO:101) of a native sequence PRO34564 cDNA, wherein SEQ ID NO:101 is a clone designated herein as "DNA216676-3083".

Figure 102 shows the amino acid sequence (SEQ ID NO:102) derived from the coding sequence of SEQ ID NO:101 shown in Figure 101.

Figure 103 shows a nucleotide sequence (SEQ ID NO:103) of a native sequence PRO35444 cDNA, wherein SEQ ID NO:103 is a clone designated herein as "DNA222653-3104".

Figure 104 shows the amino acid sequence (SEQ ID NO:104) derived from the coding sequence of SEQ ID NO:103 shown in Figure 103.

Figure 105 shows a nucleotide sequence (SEQ ID NO:105) of a native sequence PRO5998 cDNA, wherein SEQ ID NO:105 is a clone designated herein as "DNA96897-2688".

Figure 106 shows the amino acid sequence (SEQ ID NO:106) derived from the coding sequence of SEQ ID NO:105 shown in Figure 105.

Figure 107 shows a nucleotide sequence (SEQ ID NO:107) of a native sequence PRO19651 cDNA, wherein SEQ ID NO:107 is a clone designated herein as "DNA142917-3081".

Figure 108 shows the amino acid sequence (SEQ ID NO:108) derived from the coding sequence of SEQ ID NO:107 shown in Figure 107.

Figure 109 shows a nucleotide sequence (SEQ ID NO:109) of a native sequence PRO20221 cDNA, wherein SEQ ID NO:109 is a clone designated herein as "DNA142930-2914".

Figure 110 shows the amino acid sequence (SEQ ID NO:110) derived from the coding sequence of SEQ ID NO:109 shown in Figure 109.

Figure 111 shows a nucleotide sequence (SEQ ID NO:111) of a native sequence PRO21434 cDNA, wherein SEQ ID NO:111 is a clone designated herein as "DNA147253-2983".

Figure 112 shows the amino acid sequence (SEQ ID NO:112) derived from the coding sequence of SEQ ID NO:111 shown in Figure 111.

Figure 113 shows a nucleotide sequence (SEQ ID NO:113) of a native sequence PRO19822 cDNA, wherein SEQ ID NO:113 is a clone designated herein as "DNA149927-2887".

Figure 114 shows the amino acid sequence (SEQ ID NO:114) derived from the coding sequence of SEQ ID NO:113 shown in Figure 113.

## DETAILED DESCRIPTION OF THE PREFERRED EMBODIMENTS

### I. Definitions

The terms "PRO polypeptide" and "PRO" as used herein and when immediately followed by a numerical designation refer to various polypeptides, wherein the complete designation (i.e., PRO/number) refers to specific polypeptide sequences as described herein. The terms "PRO/number polypeptide" and "PRO/number" wherein the term "number" is provided as an actual numerical designation as used herein encompass native sequence polypeptides and polypeptide variants (which are further defined herein). The PRO polypeptides described herein may be isolated from a variety of sources, such as from human tissue types or from another source, or prepared by recombinant or synthetic methods. The term "PRO polypeptide" refers to each individual PRO/number polypeptide disclosed herein. All disclosures in this specification which refer to the "PRO polypeptide" refer to each of the polypeptides individually as well as jointly. For example, descriptions of the preparation of, purification of, derivation of, formation of antibodies to or against, administration of, compositions containing, treatment of a disease with, etc., pertain to each polypeptide of the invention individually. The term "PRO polypeptide" also includes variants of the PRO/number polypeptides disclosed herein.

A "native sequence PRO polypeptide" comprises a polypeptide having the same amino acid sequence as the corresponding PRO polypeptide derived from nature. Such native sequence PRO polypeptides can be isolated from nature or can be produced by recombinant or synthetic means. The term "native sequence PRO polypeptide" specifically encompasses naturally-occurring truncated or secreted forms of the specific PRO polypeptide (*e.g.*, an extracellular domain sequence), naturally-occurring variant forms (*e.g.*, alternatively spliced forms) and

naturally-occurring allelic variants of the polypeptide. In various embodiments of the invention, the native sequence PRO polypeptides disclosed herein are mature or full-length native sequence polypeptides comprising the full-length amino acids sequences shown in the accompanying figures. Start and stop codons are shown in bold font and underlined in the figures. However, while the PRO polypeptide disclosed in the accompanying figures are shown to begin with methionine residues designated herein as amino acid position 1 in the figures, it is conceivable and possible that other methionine residues located either upstream or downstream from the amino acid position 1 in the figures may be employed as the starting amino acid residue for the PRO polypeptides.

The PRO polypeptide "extracellular domain" or "ECD" refers to a form of the PRO polypeptide which is essentially free of the transmembrane and cytoplasmic domains. Ordinarily, a PRO polypeptide ECD will have less than 1 % of such transmembrane and/or cytoplasmic domains and preferably, will have less than 0.5 % of such domains. It will be understood that any transmembrane domains identified for the PRO polypeptides of the present invention are identified pursuant to criteria routinely employed in the art for identifying that type of hydrophobic domain. The exact boundaries of a transmembrane domain may vary but most likely by no more than about 5 amino acids at either end of the domain as initially identified herein. Optionally, therefore, an extracellular domain of a PRO polypeptide may contain from about 5 or fewer amino acids on either side of the transmembrane domain/extracellular domain boundary as identified in the Examples or specification and such polypeptides, with or without the associated signal peptide, and nucleic acid encoding them, are comtemplated by the present invention.

The approximate location of the "signal peptides" of the various PRO polypeptides disclosed herein are shown in the present specification and/or the accompanying figures. It is noted, however, that the C-terminal boundary of a signal peptide may vary, but most likely by no more than about 5 amino acids on either side of the signal peptide C-terminal boundary as initially identified herein, wherein the C-terminal boundary of the signal peptide may be identified pursuant to criteria routinely employed in the art for identifying that type of amino acid sequence element (e.g., Nielsen et al., Prot. Eng. 10:1-6 (1997) and von Heinje et al., Nucl. Acids. Res. 14:4683-4690 (1986)). Moreover, it is also recognized that, in some cases, cleavage of a signal sequence from a secreted polypeptide is not entirely uniform, resulting in more than one secreted species. These mature polypeptides, where the signal peptide is cleaved within no more than about 5 amino acids on either side of the C-terminal boundary of the signal peptide as identified herein, and the polynucleotides encoding them, are contemplated by the present invention.

"PRO polypeptide variant" means an active PRO polypeptide as defined above or below having at least about 80% amino acid sequence identity with a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Such PRO polypeptide variants include, for instance, PRO polypeptides wherein one or more amino acid residues are added, or deleted, at the N- or C-terminus of the full-length native amino acid sequence. Ordinarily, a PRO polypeptide variant will have at least about 80% amino acid sequence identity, alternatively at least about 81% amino acid sequence identity, alternatively at least about 82% amino acid sequence identity, alternatively at least about 83% amino acid sequence identity, alternatively

at least about 84% amino acid sequence identity, alternatively at least about 85% amino acid sequence identity, alternatively at least about 86% amino acid sequence identity, alternatively at least about 87% amino acid sequence identity, alternatively at least about 88% amino acid sequence identity, alternatively at least about 89% amino acid sequence identity, alternatively at least about 90% amino acid sequence identity, alternatively at least about 91% amino acid sequence identity, alternatively at least about 92% amino acid sequence identity, alternatively at least about 93% amino acid sequence identity, alternatively at least about 94% amino acid sequence identity, alternatively at least about 95% amino acid sequence identity, alternatively at least about 96% amino acid sequence identity, alternatively at least about 97% amino acid sequence identity, alternatively at least about 98% amino acid sequence identity and alternatively at least about 99% amino acid sequence identity to a full-length native sequence PRO polypeptide sequence as disclosed herein, a PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other specifically defined fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, PRO variant polypeptides are at least about 10 amino acids in length, alternatively at least about 20 amino acids in length, alternatively at least about 30 amino acids in length, alternatively at least about 40 amino acids in length, alternatively at least about 50 amino acids in length, alternatively at least about 60 amino acids in length, alternatively at least about 70 amino acids in length, alternatively at least about 80 amino acids in length, alternatively at least about 90 amino acids in length, alternatively at least about 100 amino acids in length, alternatively at least about 150 amino acids in length, alternatively at least about 200 amino acids in length, alternatively at least about 300 amino acids in length, or more.

"Percent (%) amino acid sequence identity" with respect to the PRO polypeptide sequences identified herein is defined as the percentage of amino acid residues in a candidate sequence that are identical with the amino acid residues in the specific PRO polypeptide sequence, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity, and not considering any conservative substitutions as part of the sequence identity. Alignment for purposes of determining percent amino acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. Those skilled in the art can determine appropriate parameters for measuring alignment, including any algorithms needed to achieve maximal alignment over the full length of the sequences being compared. For purposes herein, however, % amino acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for amino acid sequence comparisons, the % amino acid

sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A. As examples of % amino acid sequence identity calculations using this method, Tables 2 and 3 demonstrate how to calculate the % amino acid sequence identity of the amino acid sequence designated "Comparison Protein" to the amino acid sequence designated "PRO", wherein "PRO" represents the amino acid sequence of a hypothetical PRO polypeptide of interest, "Comparison Protein" represents the amino acid sequence of a polypeptide against which the "PRO" polypeptide of interest is being compared, and "X, "Y" and "Z" each represent different hypothetical amino acid residues.

Unless specifically stated otherwise, all % amino acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % amino acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % amino acid sequence identity value is determined by dividing (a) the number of matching identical amino acid residues between the amino acid sequence of the PRO polypeptide of interest having a sequence derived from the native PRO polypeptide and the comparison amino acid sequence of interest (i.e., the sequence against which the PRO polypeptide of interest is being compared which may be a PRO variant polypeptide) as determined by WU-BLAST-2 by (b) the total number of amino acid residues of the PRO polypeptide of interest. For example, in the statement "a polypeptide comprising an the amino acid sequence A which has or having at least 80% amino acid sequence identity to the amino acid sequence B", the amino acid sequence A is the comparison amino acid sequence of interest and the amino acid sequence B is the amino acid sequence of the PRO polypeptide of interest.

Percent amino acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for amino acid sequence comparisons, the % amino acid sequence identity of a given amino acid sequence A to, with, or against a given amino acid sequence B (which can alternatively be phrased as a given amino acid sequence A that has or comprises a certain % amino acid sequence identity to, with, or against a given amino acid sequence B) is calculated as follows:

100 times the fraction X/Y

where X is the number of amino acid residues scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of A and B, and where Y is the total number of amino acid residues in B. It will be appreciated that where the length of amino acid sequence A is not equal to the length of amino acid sequence B, the % amino acid sequence identity of A to B will not equal the % amino acid sequence identity of B to A.

"PRO variant polynucleotide" or "PRO variant nucleic acid sequence" means a nucleic acid molecule which encodes an active PRO polypeptide as defined below and which has at least about 80% nucleic acid sequence identity with a nucleotide acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal peptide, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Ordinarily, a PRO variant polynucleotide will have at least about 80% nucleic acid sequence identity, alternatively at least about 81% nucleic acid sequence identity, alternatively at least about 82% nucleic acid sequence identity, alternatively at least about 83% nucleic acid sequence identity, alternatively at least about 84% nucleic acid sequence identity, alternatively at least about 85% nucleic acid sequence identity, alternatively at least about 86% nucleic acid sequence identity, alternatively at least about 87% nucleic acid sequence identity, alternatively at least about 88% nucleic acid sequence identity, alternatively at least about 89% nucleic acid sequence identity, alternatively at least about 90% nucleic acid sequence identity, alternatively at least about 91% nucleic acid sequence identity, alternatively at least about 92% nucleic acid sequence identity, alternatively at least about 93% nucleic acid sequence identity, alternatively at least about 94% nucleic acid sequence identity, alternatively at least about 95% nucleic acid sequence identity, alternatively at least about 96% nucleic acid sequence identity, alternatively at least about 97% nucleic acid sequence identity, alternatively at least about 98% nucleic acid sequence identity and alternatively at least about 99% nucleic acid sequence identity with a nucleic acid sequence encoding a full-length native sequence PRO polypeptide sequence as disclosed herein, a full-length native sequence PRO polypeptide sequence lacking the signal peptide as disclosed herein, an extracellular domain of a PRO polypeptide, with or without the signal sequence, as disclosed herein or any other fragment of a full-length PRO polypeptide sequence as disclosed herein. Variants do not encompass the native nucleotide sequence.

Ordinarily, PRO variant polynucleotides are at least about 30 nucleotides in length, alternatively at least about 60 nucleotides in length, alternatively at least about 90 nucleotides in length, alternatively at least about 120 nucleotides in length, alternatively at least about 150 nucleotides in length, alternatively at least about 180 nucleotides in length, alternatively at least about 210 nucleotides in length, alternatively at least about 240

nucleotides in length, alternatively at least about 270 nucleotides in length, alternatively at least about 300 nucleotides in length, alternatively at least about 450 nucleotides in length, alternatively at least about 600 nucleotides in length, alternatively at least about 900 nucleotides in length, or more.

"Percent (%) nucleic acid sequence identity" with respect to PRO-encoding nucleic acid sequences identified herein is defined as the percentage of nucleotides in a candidate sequence that are identical with the nucleotides in the PRO nucleic acid sequence of interest, after aligning the sequences and introducing gaps, if necessary, to achieve the maximum percent sequence identity. Alignment for purposes of determining percent nucleic acid sequence identity can be achieved in various ways that are within the skill in the art, for instance, using publicly available computer software such as BLAST, BLAST-2, ALIGN or Megalign (DNASTAR) software. For purposes herein, however, % nucleic acid sequence identity values are generated using the sequence comparison computer program ALIGN-2, wherein the complete source code for the ALIGN-2 program is provided in Table 1 below. The ALIGN-2 sequence comparison computer program was authored by Genentech, Inc. and the source code shown in Table 1 below has been filed with user documentation in the U.S. Copyright Office, Washington D.C., 20559, where it is registered under U.S. Copyright Registration No. TXU510087. The ALIGN-2 program is publicly available through Genentech, Inc., South San Francisco, California or may be compiled from the source code provided in Table 1 below. The ALIGN-2 program should be compiled for use on a UNIX operating system, preferably digital UNIX V4.0D. All sequence comparison parameters are set by the ALIGN-2 program and do not vary.

In situations where ALIGN-2 is employed for nucleic acid sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program ALIGN-2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C. As examples of % nucleic acid sequence identity calculations, Tables 4 and 5, demonstrate how to calculate the % nucleic acid sequence identity of the nucleic acid sequence designated "Comparison DNA" to the nucleic acid sequence designated "PRO-DNA", wherein "PRO-DNA" represents a hypothetical PRO-encoding nucleic acid sequence of interest, "Comparison DNA" represents the nucleotide sequence of a nucleic acid molecule against which the "PRO-DNA" nucleic acid molecule of interest is being compared, and "N", "L" and "V" each represent different hypothetical nucleotides.

Unless specifically stated otherwise, all % nucleic acid sequence identity values used herein are obtained as described in the immediately preceding paragraph using the ALIGN-2 computer program. However, % nucleic acid sequence identity values may also be obtained as described below by using the WU-BLAST-2 computer

program (Altschul et al., Methods in Enzymology 266:460-480 (1996)). Most of the WU-BLAST-2 search parameters are set to the default values. Those not set to default values, i.e., the adjustable parameters, are set with the following values: overlap span = 1, overlap fraction = 0.125, word threshold (T) = 11, and scoring matrix = BLOSUM62. When WU-BLAST-2 is employed, a % nucleic acid sequence identity value is determined by dividing (a) the number of matching identical nucleotides between the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest having a sequence derived from the native sequence PRO polypeptide-encoding nucleic acid and the comparison nucleic acid molecule of interest (i.e., the sequence against which the PRO polypeptide-encoding nucleic acid molecule of interest is being compared which may be a variant PRO polynucleotide) as determined by WU-BLAST-2 by (b) the total number of nucleotides of the PRO polypeptide-encoding nucleic acid molecule of interest. For example, in the statement "an isolated nucleic acid molecule comprising a nucleic acid sequence A which has or having at least 80% nucleic acid sequence identity to the nucleic acid sequence B", the nucleic acid sequence A is the comparison nucleic acid molecule of interest and the nucleic acid sequence B is the nucleic acid sequence of the PRO polypeptide-encoding nucleic acid molecule of interest.

Percent nucleic acid sequence identity may also be determined using the sequence comparison program NCBI-BLAST2 (Altschul et al., Nucleic Acids Res. 25:3389-3402 (1997)). The NCBI-BLAST2 sequence comparison program may be downloaded from http://www.ncbi.nlm.nih.gov or otherwise obtained from the National Institute of Health, Bethesda, MD. NCBI-BLAST2 uses several search parameters, wherein all of those search parameters are set to default values including, for example, unmask = yes, strand = all, expected occurrences = 10, minimum low complexity length = 15/5, multi-pass e-value = 0.01, constant for multi-pass = 25, dropoff for final gapped alignment = 25 and scoring matrix = BLOSUM62.

In situations where NCBI-BLAST2 is employed for sequence comparisons, the % nucleic acid sequence identity of a given nucleic acid sequence C to, with, or against a given nucleic acid sequence D (which can alternatively be phrased as a given nucleic acid sequence C that has or comprises a certain % nucleic acid sequence identity to, with, or against a given nucleic acid sequence D) is calculated as follows:

100 times the fraction W/Z

where W is the number of nucleotides scored as identical matches by the sequence alignment program NCBI-BLAST2 in that program's alignment of C and D, and where Z is the total number of nucleotides in D. It will be appreciated that where the length of nucleic acid sequence C is not equal to the length of nucleic acid sequence D, the % nucleic acid sequence identity of C to D will not equal the % nucleic acid sequence identity of D to C.

In other embodiments, PRO variant polynucleotides are nucleic acid molecules that encode an active PRO polypeptide and which are capable of hybridizing, preferably under stringent hybridization and wash conditions, to nucleotide sequences encoding a full-length PRO polypeptide as disclosed herein. PRO variant polypeptides may be those that are encoded by a PRO variant polynucleotide.

"Isolated," when used to describe the various polypeptides disclosed herein, means polypeptide that has been identified and separated and/or recovered from a component of its natural environment. Contaminant

components of its natural environment are materials that would typically interfere with diagnostic or therapeutic uses for the polypeptide, and may include enzymes, hormones, and other proteinaceous or non-proteinaceous solutes. In preferred embodiments, the polypeptide will be purified (1) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (2) to homogeneity by SDS-PAGE under non-reducing or reducing conditions using Coomassie blue or, preferably, silver stain. Isolated polypeptide includes polypeptide *in situ* within recombinant cells, since at least one component of the PRO polypeptide natural environment will not be present. Ordinarily, however, isolated polypeptide will be prepared by at least one purification step.

An "isolated" PRO polypeptide-encoding nucleic acid or other polypeptide-encoding nucleic acid is a nucleic acid molecule that is identified and separated from at least one contaminant nucleic acid molecule with which it is ordinarily associated in the natural source of the polypeptide-encoding nucleic acid. An isolated polypeptide-encoding nucleic acid molecule is other than in the form or setting in which it is found in nature. Isolated polypeptide-encoding nucleic acid molecules therefore are distinguished from the specific polypeptide-encoding nucleic acid molecule as it exists in natural cells. However, an isolated polypeptide-encoding nucleic acid molecule includes polypeptide-encoding nucleic acid molecules contained in cells that ordinarily express the polypeptide where, for example, the nucleic acid molecule is in a chromosomal location different from that of natural cells.

The term "control sequences" refers to DNA sequences necessary for the expression of an operably linked coding sequence in a particular host organism. The control sequences that are suitable for prokaryotes, for example, include a promoter, optionally an operator sequence, and a ribosome binding site. Eukaryotic cells are known to utilize promoters, polyadenylation signals, and enhancers.

Nucleic acid is "operably linked" when it is placed into a functional relationship with another nucleic acid sequence. For example, DNA for a presequence or secretory leader is operably linked to DNA for a polypeptide if it is expressed as a preprotein that participates in the secretion of the polypeptide; a promoter or enhancer is operably linked to a coding sequence if it affects the transcription of the sequence; or a ribosome binding site is operably linked to a coding sequence if it is positioned so as to facilitate translation. Generally, "operably linked" means that the DNA sequences being linked are contiguous, and, in the case of a secretory leader, contiguous and in reading phase. However, enhancers do not have to be contiguous. Linking is accomplished by ligation at convenient restriction sites. If such sites do not exist, the synthetic oligonucleotide adaptors or linkers are used in accordance with conventional practice.

The term "antibody" is used in the broadest sense and specifically covers, for example, single anti-PRO monoclonal antibodies (including agonist, antagonist, and neutralizing antibodies), anti-PRO antibody compositions with polyepitopic specificity, single chain anti-PRO antibodies, and fragments of anti-PRO antibodies (see below). The term "monoclonal antibody" as used herein refers to an antibody obtained from a population of substantially homogeneous antibodies, i.e., the individual antibodies comprising the population are identical except for possible naturally-occurring mutations that may be present in minor amounts.

"Stringency" of hybridization reactions is readily determinable by one of ordinary skill in the art, and generally is an empirical calculation dependent upon probe length, washing temperature, and salt concentration.

In general, longer probes require higher temperatures for proper annealing, while shorter probes need lower temperatures. Hybridization generally depends on the ability of denatured DNA to reanneal when complementary strands are present in an environment below their melting temperature. The higher the degree of desired homology between the probe and hybridizable sequence, the higher the relative temperature which can be used. As a result, it follows that higher relative temperatures would tend to make the reaction conditions more stringent, while lower temperatures less so. For additional details and explanation of stringency of hybridization reactions, see Ausubel et al., Current Protocols in Molecular Biology, Wiley Interscience Publishers, (1995).

"Stringent conditions" or "high stringency conditions", as defined herein, may be identified by those that: (1) employ low ionic strength and high temperature for washing, for example 0.015 M sodium chloride/0.0015 M sodium citrate/0.1% sodium dodecyl sulfate at 50°C; (2) employ during hybridization a denaturing agent, such as formamide, for example, 50% (v/v) formamide with 0.1% bovine serum albumin/0.1% Ficoll/0.1% polyvinylpyrrolidone/50mM sodium phosphate buffer at pH 6.5 with 750 mM sodium chloride, 75 mM sodium citrate at 42°C; or (3) employ 50% formamide, 5 x SSC (0.75 M NaCl, 0.075 M sodium citrate), 50 mM sodium phosphate (pH 6.8), 0.1% sodium pyrophosphate, 5 x Denhardt's solution, sonicated salmon sperm DNA (50 μg/ml), 0.1% SDS, and 10% dextran sulfate at 42°C, with washes at 42°C in 0.2 x SSC (sodium chloride/sodium citrate) and 50% formamide at 55°C, followed by a high-stringency wash consisting of 0.1 x SSC containing EDTA at 55°C.

"Moderately stringent conditions" may be identified as described by Sambrook et al., Molecular Cloning: A Laboratory Manual, New York: Cold Spring Harbor Press, 1989, and include the use of washing solution and hybridization conditions (e.g., temperature, ionic strength and %SDS) less stringent that those described above. An example of moderately stringent conditions is overnight incubation at 37°C in a solution comprising: 20% formamide, 5 x SSC (150 mM NaCl, 15 mM trisodium citrate), 50 mM sodium phosphate (pH 7.6), 5 x Denhardt's solution, 10% dextran sulfate, and 20 mg/ml denatured sheared salmon sperm DNA, followed by washing the filters in 1 x SSC at about 37-50°C. The skilled artisan will recognize how to adjust the temperature, ionic strength, etc. as necessary to accommodate factors such as probe length and the like.

The term "epitope tagged" when used herein refers to a chimeric polypeptide comprising a PRO polypeptide fused to a "tag polypeptide". The tag polypeptide has enough residues to provide an epitope against which an antibody can be made, yet is short enough such that it does not interfere with activity of the polypeptide to which it is fused. The tag polypeptide preferably also is fairly unique so that the antibody does not substantially cross-react with other epitopes. Suitable tag polypeptides generally have at least six amino acid residues and usually between about 8 and 50 amino acid residues (preferably, between about 10 and 20 amino acid residues).

As used herein, the term "immunoadhesin" designates antibody-like molecules which combine the binding specificity of a heterologous protein (an "adhesin") with the effector functions of immunoglobulin constant domains. Structurally, the immunoadhesins comprise a fusion of an amino acid sequence with the desired binding specificity which is other than the antigen recognition and binding site of an antibody (i.e., is "heterologous"), and an immunoglobulin constant domain sequence. The adhesin part of an immunoadhesin molecule typically is a contiguous amino acid sequence comprising at least the binding site of a receptor or a ligand. The immunoglobulin constant domain sequence in the immunoadhesin may be obtained from any immunoglobulin,

such as IgG-1, IgG-2, IgG-3, or IgG-4 subtypes, IgA (including IgA-1 and IgA-2), IgE, IgD or IgM.

"Active" or "activity" for the purposes herein refers to form(s) of a PRO polypeptide which retain a biological and/or an immunological activity of native or naturally-occurring PRO, wherein "biological" activity refers to a biological function (either inhibitory or stimulatory) caused by a native or naturally-occurring PRO other than the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO and an "immunological" activity refers to the ability to induce the production of an antibody against an antigenic epitope possessed by a native or naturally-occurring PRO.

The term "antagonist" is used in the broadest sense, and includes any molecule that partially or fully blocks, inhibits, or neutralizes a biological activity of a native PRO polypeptide disclosed herein. In a similar manner, the term "agonist" is used in the broadest sense and includes any molecule that mimics a biological activity of a native PRO polypeptide disclosed herein. Suitable agonist or antagonist molecules specifically include agonist or antagonist antibodies or antibody fragments, fragments or amino acid sequence variants of native PRO polypeptides, peptides, antisense oligonucleotides, small organic molecules, etc. Methods for identifying agonists or antagonists of a PRO polypeptide may comprise contacting a PRO polypeptide with a candidate agonist or antagonist molecule and measuring a detectable change in one or more biological activities normally associated with the PRO polypeptide.

"Treatment" refers to both therapeutic treatment and prophylactic or preventative measures, wherein the object is to prevent or slow down (lessen) the targeted pathologic condition or disorder. Those in need of treatment include those already with the disorder as well as those prone to have the disorder or those in whom the disorder is to be prevented.

"Chronic" administration refers to administration of the agent(s) in a continuous mode as opposed to an acute mode, so as to maintain the initial therapeutic effect (activity) for an extended period of time. "Intermittent" administration is treatment that is not consecutively done without interruption, but rather is cyclic in nature.

"Mammal" for purposes of treatment refers to any animal classified as a mammal, including humans, domestic and farm animals, and zoo, sports, or pet animals, such as dogs, cats, cattle, horses, sheep, pigs, goats, rabbits, etc. Preferably, the mammal is human.

Administration "in combination with" one or more further therapeutic agents includes simultaneous (concurrent) and consecutive administration in any order.

"Carriers" as used herein include pharmaceutically acceptable carriers, excipients, or stabilizers which are nontoxic to the cell or mammal being exposed thereto at the dosages and concentrations employed. Often the physiologically acceptable carrier is an aqueous pH buffered solution. Examples of physiologically acceptable carriers include buffers such as phosphate, citrate, and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptide; proteins, such as serum albumin, gelatin, or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone; amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides, and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, polyethylene glycol (PEG), and PLURONICS™.

"Antibody fragments" comprise a portion of an intact antibody, preferably the antigen binding or variable region of the intact antibody. Examples of antibody fragments include Fab, Fab', $F(ab')_2$, and Fv fragments; diabodies; linear antibodies (Zapata et al., Protein Eng. 8(10): 1057-1062 [1995]); single-chain antibody molecules; and multispecific antibodies formed from antibody fragments.

Papain digestion of antibodies produces two identical antigen-binding fragments, called "Fab" fragments, each with a single antigen-binding site, and a residual "Fc" fragment, a designation reflecting the ability to crystallize readily. Pepsin treatment yields an $F(ab')_2$ fragment that has two antigen-combining sites and is still capable of cross-linking antigen.

"Fv" is the minimum antibody fragment which contains a complete antigen-recognition and -binding site. This region consists of a dimer of one heavy- and one light-chain variable domain in tight, non-covalent association. It is in this configuration that the three CDRs of each variable domain interact to define an antigen-binding site on the surface of the $V_H$-$V_L$ dimer. Collectively, the six CDRs confer antigen-binding specificity to the antibody. However, even a single variable domain (or half of an Fv comprising only three CDRs specific for an antigen) has the ability to recognize and bind antigen, although at a lower affinity than the entire binding site.

The Fab fragment also contains the constant domain of the light chain and the first constant domain (CH1) of the heavy chain. Fab fragments differ from Fab' fragments by the addition of a few residues at the carboxy terminus of the heavy chain CH1 domain including one or more cysteines from the antibody hinge region. Fab'-SH is the designation herein for Fab' in which the cysteine residue(s) of the constant domains bear a free thiol group. $F(ab')_2$ antibody fragments originally were produced as pairs of Fab' fragments which have hinge cysteines between them. Other chemical couplings of antibody fragments are also known.

The "light chains" of antibodies (immunoglobulins) from any vertebrate species can be assigned to one of two clearly distinct types, called kappa and lambda, based on the amino acid sequences of their constant domains.

Depending on the amino acid sequence of the constant domain of their heavy chains, immunoglobulins can be assigned to different classes. There are five major classes of immunoglobulins: IgA, IgD, IgE, IgG, and IgM, and several of these may be further divided into subclasses (isotypes), e.g., IgG1, IgG2, IgG3, IgG4, IgA, and IgA2.

"Single-chain Fv" or "sFv" antibody fragments comprise the $V_H$ and $V_L$ domains of antibody, wherein these domains are present in a single polypeptide chain. Preferably, the Fv polypeptide further comprises a polypeptide linker between the $V_H$ and $V_L$ domains which enables the sFv to form the desired structure for antigen binding. For a review of sFv, see Pluckthun in The Pharmacology of Monoclonal Antibodies, vol. 113, Rosenburg and Moore eds., Springer-Verlag, New York, pp. 269-315 (1994).

The term "diabodies" refers to small antibody fragments with two antigen-binding sites, which fragments comprise a heavy-chain variable domain ($V_H$) connected to a light-chain variable domain ($V_L$) in the same polypeptide chain ($V_H$-$V_L$). By using a linker that is too short to allow pairing between the two domains on the same chain, the domains are forced to pair with the complementary domains of another chain and create two antigen-binding sites. Diabodies are described more fully in, for example, EP 404,097; WO 93/11161; and Hollinger et al., Proc. Natl. Acad. Sci. USA, 90:6444-6448 (1993).

An "isolated" antibody is one which has been identified and separated and/or recovered from a component of its natural environment. Contaminant components of its natural environment are materials which would interfere with diagnostic or therapeutic uses for the antibody, and may include enzymes, hormones, and other proteinaceous or nonproteinaceous solutes. In preferred embodiments, the antibody will be purified (1) to greater than 95% by weight of antibody as determined by the Lowry method, and most preferably more than 99% by weight, (2) to a degree sufficient to obtain at least 15 residues of N-terminal or internal amino acid sequence by use of a spinning cup sequenator, or (3) to homogeneity by SDS-PAGE under reducing or nonreducing conditions using Coomassie blue or, preferably, silver stain. Isolated antibody includes the antibody in situ within recombinant cells since at least one component of the antibody's natural environment will not be present. Ordinarily, however, isolated antibody will be prepared by at least one purification step.

An antibody that "specifically binds to" or is "specific for" a particular polypeptide or an epitope on a particular polypeptide is one that binds to that particular polypeptide or epitope on a particular polypeptide without substantially binding to any other polypeptide or polypeptide epitope.

The word "label" when used herein refers to a detectable compound or composition which is conjugated directly or indirectly to the antibody so as to generate a "labeled" antibody. The label may be detectable by itself (e.g. radioisotope labels or fluorescent labels) or, in the case of an enzymatic label, may catalyze chemical alteration of a substrate compound or composition which is detectable.

By "solid phase" is meant a non-aqueous matrix to which the antibody of the present invention can adhere. Examples of solid phases encompassed herein include those formed partially or entirely of glass (e.g., controlled pore glass), polysaccharides (e.g., agarose), polyacrylamides, polystyrene, polyvinyl alcohol and silicones. In certain embodiments, depending on the context, the solid phase can comprise the well of an assay plate; in others it is a purification column (e.g., an affinity chromatography column). This term also includes a discontinuous solid phase of discrete particles, such as those described in U.S. Patent No. 4,275,149.

A "liposome" is a small vesicle composed of various types of lipids, phospholipids and/or surfactant which is useful for delivery of a drug (such as a PRO polypeptide or antibody thereto) to a mammal. The components of the liposome are commonly arranged in a bilayer formation, similar to the lipid arrangement of biological membranes.

A "small molecule" is defined herein to have a molecular weight below about 500 Daltons.

An "effective amount" of a polypeptide disclosed herein or an agonist or antagonist thereof is an amount sufficient to carry out a specifically stated purpose. An "effective amount" may be determined empirically and in a routine manner, in relation to the stated purpose.

## Table 1

```
/*
 *
 * C-C increased from 12 to 15
 * Z is average of EQ
 * B is average of ND
 * match with stop is _M; stop-stop = 0; J (joker) match = 0
 */
#define  _M      -8      /* value of a match with a stop */

int      _day[26][26] = {
/*     A  B  C  D  E  F  G  H  I  J  K  L  M  N  O  P  Q  R  S  T  U  V  W  X  Y  Z */
/* A */  { 2, 0,-2, 0, 0,-4, 1,-1,-1, 0,-1,-2,-1, 0,_M, 1, 0,-2, 1, 1, 0, 0,-6, 0,-3, 0},
/* B */  { 0, 3,-4, 3, 2,-5, 0, 1,-2, 0, 0,-3,-2, 2,_M,-1, 1, 0, 0, 0, 0,-2,-5, 0,-3, 1},
/* C */  {-2,-4,15,-5,-5,-4,-3,-3,-2, 0,-5,-6,-5,-4,_M,-3,-5,-4, 0,-2, 0,-2,-8, 0, 0,-5},
/* D */  { 0, 3,-5, 4, 3,-6, 1, 1,-2, 0, 0,-4,-3, 2,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 2},
/* E */  { 0, 2,-5, 3, 4,-5, 0, 1,-2, 0, 0,-3,-2, 1,_M,-1, 2,-1, 0, 0, 0,-2,-7, 0,-4, 3},
/* F */  {-4,-5,-4,-6,-5, 9,-5,-2, 1, 0,-5, 2, 0,-4,_M,-5,-5,-4,-3,-3, 0,-1, 0, 0, 7,-5},
/* G */  { 1, 0,-3, 1, 0,-5, 5,-2,-3, 0,-2,-4,-3, 0,_M,-1,-1,-3, 1, 0, 0,-1,-7, 0,-5, 0},
/* H */  {-1, 1,-3, 1, 1,-2,-2, 6,-2, 0, 0,-2,-2, 2,_M, 0, 3, 2,-1,-1, 0,-2,-3, 0, 0, 2},
/* I */  {-1,-2,-2,-2,-2, 1,-3,-2, 5, 0,-2, 2, 2,-2,_M,-2,-2,-2,-1, 0, 0, 4,-5, 0,-1,-2},
/* J */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* K */  {-1, 0,-5, 0, 0,-5,-2, 0,-2, 0, 5,-3, 0, 1,_M,-1, 1, 3, 0, 0, 0,-2,-3, 0,-4, 0},
/* L */  {-2,-3,-6,-4,-3, 2,-4,-2, 2, 0,-3, 6, 4,-3,_M,-3,-2,-3,-3,-1, 0, 2,-2, 0,-1,-2},
/* M */  {-1,-2,-5,-3,-2, 0,-3,-2, 2, 0, 0, 4, 6,-2,_M,-2,-1, 0,-2,-1, 0, 2,-4, 0,-2,-1},
/* N */  { 0, 2,-4, 2, 1,-4, 0, 2,-2, 0, 1,-3,-2, 2,_M,-1, 1, 0, 1, 0, 0,-2,-4, 0,-2, 1},
/* O */  {_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M, 0,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M,_M},
/* P */  { 1,-1,-3,-1,-1,-5,-1, 0,-2, 0,-1,-3,-2,-1,_M, 6, 0, 0, 1, 0, 0,-1,-6, 0,-5, 0},
/* Q */  { 0, 1,-5, 2, 2,-5,-1, 3,-2, 0, 1,-2,-1, 1,_M, 0, 4, 1,-1,-1, 0,-2,-5, 0,-4, 3},
/* R */  {-2, 0,-4,-1,-1,-4,-3, 2,-2, 0, 3,-3, 0, 0,_M, 0, 1, 6, 0,-1, 0,-2, 2, 0,-4, 0},
/* S */  { 1, 0, 0, 0, 0,-3, 1,-1,-1, 0, 0,-3,-2, 1,_M, 1,-1, 0, 2, 1, 0,-1,-2, 0,-3, 0},
/* T */  { 1, 0,-2, 0, 0,-3, 0,-1, 0, 0, 0,-1,-1, 0,_M, 0,-1,-1, 1, 3, 0, 0,-5, 0,-3, 0},
/* U */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* V */  { 0,-2,-2,-2,-2,-1,-1,-2, 4, 0,-2, 2, 2,-2,_M,-1,-2,-2,-1, 0, 0, 4,-6, 0,-2,-2},
/* W */  {-6,-5,-8,-7,-7, 0,-7,-3,-5, 0,-3,-2,-4,-4,_M,-6,-5, 2,-2,-5, 0,-6,17, 0, 0,-6},
/* X */  { 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,_M, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0},
/* Y */  {-3,-3, 0,-4,-4, 7,-5, 0,-1, 0,-4,-1,-2,-2,_M,-5,-4,-4,-3,-3, 0,-2, 0, 0,10,-4},
/* Z */  { 0, 1,-5, 2, 3,-5, 0, 2,-2, 0, 0,-2,-1, 1,_M, 0, 3, 0, 0, 0, 0,-2,-6, 0,-4, 4}
};
```

## Table 1 (cont')

```
/*
 */
#include <stdio.h>
#include <ctype.h>

#define  MAXJMP      16      /* max jumps in a diag */
#define  MAXGAP      24      /* don't continue to penalize gaps larger than this */
#define  JMPS        1024    /* max jmps in an path */
#define  MX          4       /* save if there's at least MX-1 bases since last jmp */

#define  DMAT        3       /* value of matching bases */
#define  DMIS        0       /* penalty for mismatched bases */
#define  DINS0       8       /* penalty for a gap */
#define  DINS1       1       /* penalty per base */
#define  PINS0       8       /* penalty for a gap */
#define  PINS1       4       /* penalty per residue */

struct jmp {
        short           n[MAXJMP];      /* size of jmp (neg for dely) */
        unsigned short  x[MAXJMP];      /* base no. of jmp in seq x */
};                                      /* limits seq to 2^16 -1 */

struct diag {
        int             score;          /* score at last jmp */
        long            offset;         /* offset of prev block */
        short           ijmp;           /* current jmp index */
        struct jmp      jp;             /* list of jmps */
};

struct path {
        int     spc;            /* number of leading spaces */
        short   n[JMPS];/* size of jmp (gap) */
        int     x[JMPS];/* loc of jmp (last elem before gap) */
};

char            *ofile;                 /* output file name */
char            *namex[2];              /* seq names: getseqs() */
char            *prog;                  /* prog name for err msgs */
char            *seqx[2];               /* seqs: getseqs() */
int             dmax;                   /* best diag: nw() */
int             dmax0;                  /* final diag */
int             dna;                    /* set if dna: main() */
int             endgaps;                /* set if penalizing end gaps */
int             gapx, gapy;             /* total gaps in seqs */
int             len0, len1;             /* seq lens */
int             ngapx, ngapy;           /* total size of gaps */
int             smax;                   /* max score: nw() */
int             *xbm;                   /* bitmap for matching */
long            offset;                 /* current offset in jmp file */
struct  diag    *dx;                    /* holds diagonals */
struct  path    pp[2];                  /* holds path for seqs */

char            *calloc(), *malloc(), *index(), *strcpy();
char            *getseq(), *g_calloc();
```

## Table 1 (cont')

```
/* Needleman-Wunsch alignment program
 *
 * usage: progs file1 file2
 *  where file1 and file2 are two dna or two protein sequences.
 *  The sequences can be in upper- or lower-case an may contain ambiguity
 *  Any lines beginning with ';', '>' or '<' are ignored
 *  Max file length is 65535 (limited by unsigned short x in the jmp struct)
 *  A sequence with 1/3 or more of its elements ACGTU is assumed to be DNA
 *  Output is in the file "align.out"
 *
 * The program may create a tmp file in /tmp to hold info about traceback.
 * Original version developed under BSD 4.3 on a vax 8650
 */
#include "nw.h"
#include "day.h"

static  _dbval[26] = {
        1,14,2,13,0,0,4,11,0,0,12,0,3,15,0,0,0,5,6,8,8,7,9,0,10,0
};

static  _pbval[26] = {
        1, 2|(1<<('D'-'A'))|(1<<('N'-'A')), 4, 8, 16, 32, 64,
        128, 256, 0xFFFFFFFF, 1<<10, 1<<11, 1<<12, 1<<13, 1<<14,
        1<<15, 1<<16, 1<<17, 1<<18, 1<<19, 1<<20, 1<<21, 1<<22,
        1<<23, 1<<24, 1<<25|(1<<('E'-'A'))|(1<<('Q'-'A'))
};

main(ac, av)                                                    main
        int     ac;
        char    *av[];
{
        prog = av[0];
        if (ac != 3) {
                fprintf(stderr,"usage: %s file1 file2\n", prog);
                fprintf(stderr,"where file1 and file2 are two dna or two protein sequences.\n");
                fprintf(stderr,"The sequences can be in upper- or lower-case\n");
                fprintf(stderr,"Any lines beginning with ';' or '<' are ignored\n");
                fprintf(stderr,"Output is in the file \"align.out\"\n");
                exit(1);
        }
        namex[0] = av[1];
        namex[1] = av[2];
        seqx[0] = getseq(namex[0], &len0);
        seqx[1] = getseq(namex[1], &len1);
        xbm = (dna)? _dbval : _pbval;

        endgaps = 0;                    /* 1 to penalize endgaps */
        ofile = "align.out";            /* output file */

        nw();           /* fill in the matrix, get the possible jmps */
        readjmps();     /* get the actual jmps */
        print();        /* print stats, alignment */

        cleanup(0);     /* unlink any tmp files */
}
```

## Table 1 (cont')

```
/* do the alignment, return best score: main()
 * dna: values in Fitch and Smith, PNAS, 80, 1382-1386, 1983
 * pro: PAM 250 values
 * When scores are equal, we prefer mismatches to any gap, prefer
 * a new gap to extending an ongoing gap, and prefer a gap in seqx
 * to a gap in seq y.
 */
nw()                                                                    nw
{
        char            *px, *py;       /* seqs and ptrs */
        int             *ndely, *dely;  /* keep track of dely */
        int             ndelx, delx;    /* keep track of delx */
        int             *tmp;           /* for swapping row0, row1 */
        int             mis;            /* score for each type */
        int             ins0, ins1;     /* insertion penalties */
        register        id;             /* diagonal index */
        register        ij;             /* jmp index */
        register        *col0, *col1;   /* score for curr, last row */
        register        xx, yy;         /* index into seqs */

        dx = (struct diag *)g_calloc("to get diags", len0+len1+1, sizeof(struct diag));

        ndely = (int *)g_calloc("to get ndely", len1+1, sizeof(int));
        dely = (int *)g_calloc("to get dely", len1+1, sizeof(int));
        col0 = (int *)g_calloc("to get col0", len1+1, sizeof(int));
        col1 = (int *)g_calloc("to get col1", len1+1, sizeof(int));
        ins0 = (dna)? DINS0 : PINS0;
        ins1 = (dna)? DINS1 : PINS1;

        smax = -10000;
        if (endgaps) {
                for (col0[0] = dely[0] = -ins0, yy = 1; yy <= len1; yy++) {
                        col0[yy] = dely[yy] = col0[yy-1] - ins1;
                        ndely[yy] = yy;
                }
                col0[0] = 0;            /* Waterman Bull Math Biol 84 */
        }
        else
                for (yy = 1; yy <= len1; yy++)
                        dely[yy] = -ins0;

        /* fill in match matrix
         */
        for (px = seqx[0], xx = 1; xx <= len0; px++, xx++) {
                /* initialize first entry in col
                 */
                if (endgaps) {
                        if (xx == 1)
                                col1[0] = delx = -(ins0+ins1);
                        else
                                col1[0] = delx = col0[0] - ins1;
                        ndelx = xx;
                }
                else {
                        col1[0] = 0;
                        delx = -ins0;
                        ndelx = 0;
                }
```

## Table 1 (cont')

...nw

```
for (py = seqx[1], yy = 1; yy <= len1; py++, yy++) {
        mis = col0[yy-1];
        if (dna)
                mis += (xbm[*px-'A']&xbm[*py-'A'])? DMAT : DMIS;
        else
                mis += _day[*px-'A'][*py-'A'];

        /* update penalty for del in x seq;
         * favor new del over ongong del
         * ignore MAXGAP if weighting endgaps
         */
        if (endgaps || ndely[yy] < MAXGAP) {
                if (col0[yy] - ins0 >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else {
                        dely[yy] -= ins1;
                        ndely[yy]++;
                }
        } else {
                if (col0[yy] - (ins0+ins1) >= dely[yy]) {
                        dely[yy] = col0[yy] - (ins0+ins1);
                        ndely[yy] = 1;
                } else
                        ndely[yy]++;
        }

        /* update penalty for del in y seq;
         * favor new del over ongong del
         */
        if (endgaps || ndelx < MAXGAP) {
                if (col1[yy-1] - ins0 >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else {
                        delx -= ins1;
                        ndelx++;
                }
        } else {
                if (col1[yy-1] - (ins0+ins1) >= delx) {
                        delx = col1[yy-1] - (ins0+ins1);
                        ndelx = 1;
                } else
                        ndelx++;
        }

        /* pick the maximum score; we're favoring
         * mis over any del and delx over dely
         */
```

## Table 1 (cont')

...nw

```
                id = xx - yy + len1 - 1;
                if (mis >= delx && mis >= dely[yy])
                        col1[yy] = mis;
                else if (delx >= dely[yy]) {
                        col1[yy] = delx;
                        ij = dx[id].ijmp;
                        if (dx[id].jp.n[0] && (!dna  || (ndelx >= MAXJMP
                        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                                dx[id].ijmp++;
                                if (++ij >= MAXJMP) {
                                        writejmps(id);
                                        ij = dx[id].ijmp = 0;
                                        dx[id].offset = offset;
                                        offset += sizeof(struct jmp) + sizeof(offset);
                                }
                        }
                        dx[id].jp.n[ij] = ndelx;
                        dx[id].jp.x[ij] = xx;
                        dx[id].score = delx;
                }
                else {
                        col1[yy] = dely[yy];
                        ij = dx[id].ijmp;
        if (dx[id].jp.n[0] && (!dna || (ndely[yy] >= MAXJMP
                        && xx > dx[id].jp.x[ij]+MX) || mis > dx[id].score+DINS0)) {
                                dx[id].ijmp++;
                                if (++ij >= MAXJMP) {
                                        writejmps(id);
                                        ij = dx[id].ijmp = 0;
                                        dx[id].offset = offset;
                                        offset += sizeof(struct jmp) + sizeof(offset);
                                }
                        }
                        dx[id].jp.n[ij] = -ndely[yy];
                        dx[id].jp.x[ij] = xx;
                        dx[id].score = dely[yy];
                }
                if (xx == len0 && yy < len1) {
                        /* last col
                         */
                        if (endgaps)
                                col1[yy] -= ins0+ins1*(len1-yy);
                        if (col1[yy] > smax) {
                                smax = col1[yy];
                                dmax = id;
                        }
                }
        }
        if (endgaps && xx < len0)
                col1[yy-1] -= ins0+ins1*(len0-xx);
        if (col1[yy-1] > smax) {
                smax = col1[yy-1];
                dmax = id;
        }
        tmp = col0; col0 = col1; col1 = tmp;
}
(void) free((char *)ndely);
(void) free((char *)dely);
(void) free((char *)col0);
(void) free((char *)col1);                      }
```

## Table 1 (cont')

```
/*
 *
 * print() -- only routine visible outside this module
 *
 * static:
 * getmat() -- trace back best path, count matches: print()
 * pr_align() -- print alignment of described in array p[]: print()
 * dumpblock() -- dump a block of lines with numbers, stars: pr_align()
 * nums() -- put out a number line: dumpblock()
 * putline() -- put out a line (name, [num], seq, [num]): dumpblock()
 * stars() - -put a line of stars: dumpblock()
 * stripname() -- strip any path and prefix from a seqname
 */

#include "nw.h"

#define SPC     3
#define P_LINE  256     /* maximum output line */
#define P_SPC   3       /* space between name or num and seq */

extern  _day[26][26];
int     olen;           /* set output line length */
FILE    *fx;            /* output file */

print()                                                          print
{
        int     lx, ly, firstgap, lastgap;      /* overlap */

        if ((fx = fopen(ofile, "w")) == 0) {
                fprintf(stderr,"%s: can't write %s\n", prog, ofile);
                cleanup(1);
        }
        fprintf(fx, "<first sequence: %s (length = %d)\n", namex[0], len0);
        fprintf(fx, "<second sequence: %s (length = %d)\n", namex[1], len1);
        olen = 60;
        lx = len0;
        ly = len1;
        firstgap = lastgap = 0;
        if (dmax < len1 - 1) {          /* leading gap in x */
                pp[0].spc = firstgap = len1 - dmax - 1;
                ly -= pp[0].spc;
        }
        else if (dmax > len1 - 1) {     /* leading gap in y */
                pp[1].spc = firstgap = dmax - (len1 - 1);
                lx -= pp[1].spc;
        }
        if (dmax0 < len0 - 1) {         /* trailing gap in x */
                lastgap = len0 - dmax0 -1;
                lx -= lastgap;
        }
        else if (dmax0 > len0 - 1) {    /* trailing gap in y */
                lastgap = dmax0 - (len0 - 1);
                ly -= lastgap;
        }
        getmat(lx, ly, firstgap, lastgap);
        pr_align();
}
```

## Table 1 (cont')

```
/*
 * trace back the best path, count matches
 */
static
getmat(lx, ly, firstgap, lastgap)                                    getmat
        int     lx, ly;                 /* "core" (minus endgaps) */
        int     firstgap, lastgap;      /* leading trailing overlap */
{
        int             nm, i0, i1, siz0, siz1;
        char            outx[32];
        double          pct;
        register        n0, n1;
        register char   *p0, *p1;

        /* get total matches, score
         */
        i0 = i1 = siz0 = siz1 = 0;
        p0 = seqx[0] + pp[1].spc;
        p1 = seqx[1] + pp[0].spc;
        n0 = pp[1].spc + 1;
        n1 = pp[0].spc + 1;

        nm = 0;
        while ( *p0 && *p1 ) {
                if (siz0) {
                        p1++;
                        n1++;
                        siz0--;
                }
                else if (siz1) {
                        p0++;
                        n0++;
                        siz1--;
                }
                else {
                        if (xbm[*p0-'A']&xbm[*p1-'A'])
                                nm++;
                        if (n0++ == pp[0].x[i0])
                                siz0 = pp[0].n[i0++];
                        if (n1++ == pp[1].x[i1])
                                siz1 = pp[1].n[i1++];
                        p0++;
                        p1++;
                }
        }

        /* pct homology:
         * if penalizing endgaps, base is the shorter seq
         * else, knock off overhangs and take shorter core
         */
        if (endgaps)
                lx = (len0 < len1)? len0 : len1;
        else
                lx = (lx < ly)? lx : ly;
        pct = 100.*(double)nm/(double)lx;
        fprintf(fx, "\n");
        fprintf(fx, "< %d match%s in an overlap of %d: %.2f percent similarity\n",
                nm, (nm == 1)? "" : "es", lx, pct);
```

## Table 1 (cont')

```
        fprintf(fx, "<gaps in first sequence: %d", gapx);                    ...getmat
        if (gapx) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapx, (dna)? "base":"residue", (ngapx == 1)? "":"s");
                fprintf(fx,"%s", outx);
        }
        fprintf(fx, ", gaps in second sequence: %d", gapy);
        if (gapy) {
                (void) sprintf(outx, " (%d %s%s)",
                        ngapy, (dna)? "base":"residue", (ngapy == 1)? "":"s");
                fprintf(fx,"%s", outx);
        }
        if (dna)
                fprintf(fx,
                "\n<score: %d (match = %d, mismatch = %d, gap penalty = %d + %d per base)\n",
                smax, DMAT, DMIS, DINS0, DINS1);
        else
                fprintf(fx,
                "\n<score: %d (Dayhoff PAM 250 matrix, gap penalty = %d + %d per residue)\n",
                smax, PINS0, PINS1);
        if (endgaps)
                fprintf(fx,
                "<endgaps penalized. left endgap: %d %s%s, right endgap: %d %s%s\n",
                firstgap, (dna)? "base" : "residue", (firstgap == 1)? "" : "s",
                lastgap, (dna)? "base" : "residue", (lastgap == 1)? "" : "s");
        else
                fprintf(fx, "<endgaps not penalized\n");
}

static          nm;             /* matches in core -- for checking */
static          lmax;           /* lengths of stripped file names */
static          ij[2];          /* jmp index for a path */
static          nc[2];          /* number at start of current line */
static          ni[2];          /* current elem number -- for gapping */
static          siz[2];
static char     *ps[2];         /* ptr to current element */
static char     *po[2];         /* ptr to next output char slot */
static char     out[2][P_LINE]; /* output line */
static char     star[P_LINE];   /* set by stars() */

/*
 * print alignment of described in struct path pp[]
 */
static
pr_align()                                                                   pr_align
{
        int             nn;     /* char count */
        int             more;
        register        i;

        for (i = 0, lmax = 0; i < 2; i++) {
                nn = stripname(namex[i]);
                if (nn > lmax)
                        lmax = nn;

                nc[i] = 1;
                ni[i] = 1;
                siz[i] = ij[i] = 0;
                ps[i] = seqx[i];
                po[i] = out[i];                 }
```

## Table 1 (cont')

...pr_align

```
        for (nn = nm = 0, more = 1; more; ) {
                for (i = more = 0; i < 2; i++) {
                        /*
                         * do we have more of this sequence?
                         */
                        if (!*ps[i])
                                continue;

                        more++;

                        if (pp[i].spc) {      /* leading space */
                                *po[i]++ = ' ';
                                pp[i].spc--;
                        }
                        else if (siz[i]) {    /* in a gap */
                                *po[i]++ = '-';
                                siz[i]--;
                        }
                        else {                /* we're putting a seq element
                                               */
                                *po[i] = *ps[i];
                                if (islower(*ps[i]))
                                        *ps[i] = toupper(*ps[i]);
                                po[i]++;
                                ps[i]++;

                                /*
                                 * are we at next gap for this seq?
                                 */
                                if (ni[i] == pp[i].x[ij[i]]) {
                                        /*
                                         * we need to merge all gaps
                                         * at this location
                                         */
                                        siz[i] = pp[i].n[ij[i]++];
                                        while (ni[i] == pp[i].x[ij[i]])
                                                siz[i] += pp[i].n[ij[i]++];
                                }
                                ni[i]++;
                        }
                }
                if (++nn == olen || !more && nn) {
                        dumpblock();
                        for (i = 0; i < 2; i++)
                                po[i] = out[i];
                        nn = 0;
                }
        }
}

/*
 * dump a block of lines, including numbers, stars: pr_align()
 */
static
dumpblock()
{
        register  i;

        for (i = 0; i < 2; i++)
                *po[i]-- = '\0';
```

dumpblock

## Table 1 (cont')

...dumpblock

```
        (void) putc('\n', fx);
        for (i = 0; i < 2; i++) {
                if (*out[i] && (*out[i] != ' ' || *(po[i]) != ' ')) {
                        if (i == 0)
                                nums(i);
                        if (i == 0 && *out[1])
                                stars();
                        putline(i);
                        if (i == 0 && *out[1])
                                fprintf(fx, star);
                        if (i == 1)
                                nums(i);
                }
        }
}

/*
 * put out a number line: dumpblock()
 */
static
nums(ix)                                                        nums
        int     ix;     /* index in out[] holding seq line */
{
        char            nline[P_LINE];
        register        i, j;
        register char   *pn, *px, *py;

        for (pn = nline, i = 0; i < lmax+P_SPC; i++, pn++)
                *pn = ' ';
        for (i = nc[ix], py = out[ix]; *py; py++, pn++) {
                if (*py == ' ' || *py == '-')
                        *pn = ' ';
                else {
                        if (i%10 == 0 || (i == 1 && nc[ix] != 1)) {
                                j = (i < 0)? -i : i;
                                for (px = pn; j; j /= 10, px--)
                                        *px = j%10 + '0';
                                if (i < 0)
                                        *px = '-';
                        }
                        else
                                *pn = ' ';
                        i++;
                }
        }
        *pn = '\0';
        nc[ix] = i;
        for (pn = nline; *pn; pn++)
                (void) putc(*pn, fx);
        (void) putc('\n', fx);
}

/*
 * put out a line (name, [num], seq, [num]): dumpblock()
 */
static
putline(ix)                                                     putline
        int     ix;                     {
```

## Table 1 (cont')

...putline

```
        int             i;
        register char   *px;

        for (px = namex[ix], i = 0; *px && *px != ':'; px++, i++)
                (void) putc(*px, fx);
        for (; i < lmax+P_SPC; i++)
                (void) putc(' ', fx);

        /* these count from 1:
         * ni[] is current element (from 1)
         * nc[] is number at start of current line
         */
        for (px = out[ix]; *px; px++)
                (void) putc(*px&0x7F, fx);
        (void) putc('\n', fx);
}

/*
 * put a line of stars (seqs always in out[0], out[1]): dumpblock()
 */
static
stars()                                                          stars
{
        int             i;
        register char   *p0, *p1, cx, *px;

        if (!*out[0] || (*out[0] == ' ' && *(po[0]) == ' ') ||
           !*out[1] || (*out[1] == ' ' && *(po[1]) == ' '))
                return;
        px = star;
        for (i = lmax+P_SPC; i; i--)
                *px++ = ' ';

        for (p0 = out[0], p1 = out[1]; *p0 && *p1; p0++, p1++) {
                if (isalpha(*p0) && isalpha(*p1)) {

                        if (xbm[*p0-'A']&xbm[*p1-'A']) {
                                cx = '*';
                                nm++;
                        }
                        else if (!dna && _day[*p0-'A'][*p1-'A'] > 0)
                                cx = '.';
                        else
                                cx = ' ';
                }
                else
                        cx = ' ';
                *px++ = cx;
        }
        *px++ = '\n';
        *px = '\0';
}
```

## Table 1 (cont')

```
/*
 * strip path or prefix from pn, return len: pr_align()
 */
static
stripname(pn)                                                    stripname
        char    *pn;    /* file name (may be path) */
{
        register char   *px, *py;

        py = 0;
        for (px = pn; *px; px++)
                if (*px == '/')
                        py = px + 1;
        if (py)
                (void) strcpy(pn, py);
        return(strlen(pn));

}
```

## Table 1 (cont')

```
/*
 * cleanup() -- cleanup any tmp file
 * getseq() -- read in seq, set dna, len, maxlen
 * g_calloc() -- calloc() with error checkin
 * readjmps() -- get the good jmps, from tmp file if necessary
 * writejmps() -- write a filled array of jmps to a tmp file: nw()
 */
#include "nw.h"
#include <sys/file.h>

char    *jname = "/tmp/homgXXXXXX";             /* tmp file for jmps */
FILE    *fj;

int     cleanup();                              /* cleanup tmp file */
long    lseek();

/*
 * remove any tmp file if we blow
 */
cleanup(i)                                                          cleanup
        int     i;
{
        if (fj)
                (void) unlink(jname);
        exit(i);
}

/*
 * read, return ptr to seq, set dna, len, maxlen
 * skip lines starting with ';', '<', or '>'
 * seq in upper or lower case
 */
char    *
getseq(file, len)                                                   getseq
        char    *file;  /* file name */
        int     *len;   /* seq len */
{
        char            line[1024], *pseq;
        register char   *px, *py;
        int             natgc, tlen;
        FILE            *fp;

        if ((fp = fopen(file,"r")) == 0) {
                fprintf(stderr,"%s: can't read %s\n", prog, file);
                exit(1);
        }
        tlen = natgc = 0;
        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++)
                        if (isupper(*px) || islower(*px))
                                tlen++;
        }
        if ((pseq = malloc((unsigned)(tlen+6))) == 0) {
                fprintf(stderr,"%s: malloc() failed to get %d bytes for %s\n", prog, tlen+6, file);
                exit(1);
        }
        pseq[0] = pseq[1] = pseq[2] = pseq[3] = '\0';
```

## Table 1 (cont')

...getseq

```
        py = pseq + 4;
        *len = tlen;
        rewind(fp);

        while (fgets(line, 1024, fp)) {
                if (*line == ';' || *line == '<' || *line == '>')
                        continue;
                for (px = line; *px != '\n'; px++) {
                        if (isupper(*px))
                                *py++ = *px;
                        else if (islower(*px))
                                *py++ = toupper(*px);
                        if (index("ATGCU",*(py-1)))
                                natgc++;
                }
        }
        *py++ = '\0';
        *py = '\0';
        (void) fclose(fp);
        dna = natgc > (tlen/3);
        return(pseq+4);
}

char    *
g_calloc(msg, nx, sz)                                                    g_calloc
        char    *msg;           /* program, calling routine */
        int     nx, sz;         /* number and size of elements */
{
        char            *px, *calloc();

        if ((px = calloc((unsigned)nx, (unsigned)sz)) == 0) {
                if (*msg) {
                        fprintf(stderr, "%s: g_calloc() failed %s (n=%d, sz=%d)\n", prog, msg, nx, sz);
                        exit(1);
                }
        }
        return(px);
}

/*
 * get final jmps from dx[] or tmp file, set pp[], reset dmax: main()
 */
readjmps()                                                               readjmps
{
        int             fd = -1;
        int             siz, i0, i1;
        register  i, j, xx;

        if (fj) {
                (void) fclose(fj);
                if ((fd = open(jname, O_RDONLY, 0)) < 0) {
                        fprintf(stderr, "%s: can't open() %s\n", prog, jname);
                        cleanup(1);
                }
        }
        for (i = i0 = i1 = 0, dmax0 = dmax, xx = len0; ; i++) {
                while (1) {
                        for (j = dx[dmax].ijmp; j >= 0 && dx[dmax].jp.x[j] >= xx; j--)
                                ;
```

## Table 1 (cont')

...readjmps

```
                        if (j < 0 && dx[dmax].offset && fj) {
                                (void) lseek(fd, dx[dmax].offset, 0);
                                (void) read(fd, (char *)&dx[dmax].jp, sizeof(struct jmp));
                                (void) read(fd, (char *)&dx[dmax].offset, sizeof(dx[dmax].offset));
                                dx[dmax].ijmp = MAXJMP-1;
                        }
                        else
                                break;
                }
                if (i >= JMPS) {
                        fprintf(stderr, "%s: too many gaps in alignment\n", prog);
                        cleanup(1);
                }
                if (j >= 0) {
                        siz = dx[dmax].jp.n[j];
                        xx = dx[dmax].jp.x[j];
                        dmax += siz;
                        if (siz < 0) {                  /* gap in second seq */
                                pp[1].n[i1] = -siz;
                                xx += siz;
                                /* id = xx - yy + len1 - 1
                                 */
                                pp[1].x[i1] = xx - dmax + len1 - 1;
                                gapy++;
                                ngapy -= siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (-siz < MAXGAP || endgaps)? -siz : MAXGAP;
                                i1++;
                        }
                        else if (siz > 0) {  /* gap in first seq */
                                pp[0].n[i0] = siz;
                                pp[0].x[i0] = xx;
                                gapx++;
                                ngapx += siz;
/* ignore MAXGAP when doing endgaps */
                                siz = (siz < MAXGAP || endgaps)? siz : MAXGAP;
                                i0++;
                        }
                }
                else
                        break;
        }

        /* reverse the order of jmps
         */
        for (j = 0, i0--; j < i0; j++, i0--) {
                i = pp[0].n[j]; pp[0].n[j] = pp[0].n[i0]; pp[0].n[i0] = i;
                i = pp[0].x[j]; pp[0].x[j] = pp[0].x[i0]; pp[0].x[i0] = i;
        }
        for (j = 0, i1--; j < i1; j++, i1--) {
                i = pp[1].n[j]; pp[1].n[j] = pp[1].n[i1]; pp[1].n[i1] = i;
                i = pp[1].x[j]; pp[1].x[j] = pp[1].x[i1]; pp[1].x[i1] = i;
        }
        if (fd >= 0)
                (void) close(fd);
        if (fj) {
                (void) unlink(jname);
                fj = 0;
                offset = 0;
        }                                       }
```

## Table 1 (cont')

writejmps

```
/*
 * write a filled jmp struct offset of the prev one (if any): nw()
 */
writejmps(ix)
        int     ix;
{
        char    *mktemp();

        if (!fj) {
                if (mktemp(jname) < 0) {
                        fprintf(stderr, "%s: can't mktemp() %s\n", prog, jname);
                        cleanup(1);
                }
                if ((fj = fopen(jname, "w")) == 0) {
                        fprintf(stderr, "%s: can't write %s\n", prog, jname);
                        exit(1);
                }
        }
        (void) fwrite((char *)&dx[ix].jp, sizeof(struct jmp), 1, fj);
        (void) fwrite((char *)&dx[ix].offset, sizeof(dx[ix].offset), 1, fj);
}
```

## Table 2

| | | |
|---|---|---|
| PRO | XXXXXXXXXXXXXXX | (Length = 15 amino acids) |
| Comparison Protein | XXXXXYYYYYYY | (Length = 12 amino acids) |

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 15 = 33.3%

## Table 3

| | | |
|---|---|---|
| PRO | XXXXXXXXXX | (Length = 10 amino acids) |
| Comparison Protein | XXXXXYYYYYYZZYZ | (Length = 15 amino acids) |

% amino acid sequence identity =

(the number of identically matching amino acid residues between the two polypeptide sequences as determined by ALIGN-2) divided by (the total number of amino acid residues of the PRO polypeptide) =

5 divided by 10 = 50%

## Table 4

| | | |
|---|---|---|
| PRO-DNA | NNNNNNNNNNNNN | (Length = 14 nucleotides) |
| Comparison DNA | NNNNNNLLLLLLLLL | (Length = 16 nucleotides) |

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

6 divided by 14 = 42.9%

Table 5

| | | |
|---|---|---|
| PRO-DNA | NNNNNNNNNNN | (Length = 12 nucleotides) |
| Comparison DNA | NNNNLLLVV | (Length = 9 nucleotides) |

% nucleic acid sequence identity =

(the number of identically matching nucleotides between the two nucleic acid sequences as determined by ALIGN-2) divided by (the total number of nucleotides of the PRO-DNA nucleic acid sequence) =

4 divided by 12 = 33.3%

II. Compositions and Methods of the Invention

A. Full-Length PRO Polypeptides

The present invention provides newly identified and isolated nucleotide sequences encoding polypeptides referred to in the present application as PRO polypeptides. In particular, cDNAs encoding various PRO polypeptides have been identified and isolated, as disclosed in further detail in the Examples below. It is noted that proteins produced in separate expression rounds may be given different PRO numbers but the UNQ number is unique for any given DNA and the encoded protein, and will not be changed. However, for sake of simplicity, in the present specification the protein encoded by the full length native nucleic acid molecules disclosed herein as well as all further native homologues and variants included in the foregoing definition of PRO, will be referred to as "PRO/number", regardless of their origin or mode of preparation.

As disclosed in the Examples below, various cDNA clones have been deposited with the ATCC. The actual nucleotide sequences of those clones can readily be determined by the skilled artisan by sequencing of the deposited clone using routine methods in the art. The predicted amino acid sequence can be determined from the nucleotide sequence using routine skill. For the PRO polypeptides and encoding nucleic acids described herein, Applicants have identified what is believed to be the reading frame best identifiable with the sequence information available at the time.

B. PRO Polypeptide Variants

In addition to the full-length native sequence PRO polypeptides described herein, it is contemplated that PRO variants can be prepared. PRO variants can be prepared by introducing appropriate nucleotide changes into the PRO DNA, and/or by synthesis of the desired PRO polypeptide. Those skilled in the art will appreciate that amino acid changes may alter post-translational processes of the PRO, such as changing the number or position of glycosylation sites or altering the membrane anchoring characteristics.

Variations in the native full-length sequence PRO or in various domains of the PRO described herein, can be made, for example, using any of the techniques and guidelines for conservative and non-conservative

mutations set forth, for instance, in U.S. Patent No. 5,364,934. Variations may be a substitution, deletion or insertion of one or more codons encoding the PRO that results in a change in the amino acid sequence of the PRO as compared with the native sequence PRO. Optionally the variation is by substitution of at least one amino acid with any other amino acid in one or more of the domains of the PRO. Guidance in determining which amino acid residue may be inserted, substituted or deleted without adversely affecting the desired activity may be found by comparing the sequence of the PRO with that of homologous known protein molecules and minimizing the number of amino acid sequence changes made in regions of high homology. Amino acid substitutions can be the result of replacing one amino acid with another amino acid having similar structural and/or chemical properties, such as the replacement of a leucine with a serine, i.e., conservative amino acid replacements. Insertions or deletions may optionally be in the range of about 1 to 5 amino acids. The variation allowed may be determined by systematically making insertions, deletions or substitutions of amino acids in the sequence and testing the resulting variants for activity exhibited by the full-length or mature native sequence.

PRO polypeptide fragments are provided herein. Such fragments may be truncated at the N-terminus or C-terminus, or may lack internal residues, for example, when compared with a full length native protein. Certain fragments lack amino acid residues that are not essential for a desired biological activity of the PRO polypeptide.

PRO fragments may be prepared by any of a number of conventional techniques. Desired peptide fragments may be chemically synthesized. An alternative approach involves generating PRO fragments by enzymatic digestion, e.g., by treating the protein with an enzyme known to cleave proteins at sites defined by particular amino acid residues, or by digesting the DNA with suitable restriction enzymes and isolating the desired fragment. Yet another suitable technique involves isolating and amplifying a DNA fragment encoding a desired polypeptide fragment, by polymerase chain reaction (PCR). Oligonucleotides that define the desired termini of the DNA fragment are employed at the 5' and 3' primers in the PCR. Preferably, PRO polypeptide fragments share at least one biological and/or immunological activity with the native PRO polypeptide disclosed herein.

In particular embodiments, conservative substitutions of interest are shown in Table 6 under the heading of preferred substitutions. If such substitutions result in a change in biological activity, then more substantial changes, denominated exemplary substitutions in Table 6, or as further described below in reference to amino acid classes, are introduced and the products screened.

Table 6

| Original Residue | Exemplary Substitutions | Preferred Substitutions |
|---|---|---|
| Ala (A) | val; leu; ile | val |
| Arg (R) | lys; gln; asn | lys |
| Asn (N) | gln; his; lys; arg | gln |
| Asp (D) | glu | glu |
| Cys (C) | ser | ser |
| Gln (Q) | asn | asn |
| Glu (E) | asp | asp |
| Gly (G) | pro; ala | ala |
| His (H) | asn; gln; lys; arg | arg |
| Ile (I) | leu; val; met; ala; phe; norleucine | leu |
| Leu (L) | norleucine; ile; val; met; ala; phe | ile |
| Lys (K) | arg; gln; asn | arg |
| Met (M) | leu; phe; ile | leu |
| Phe (F) | leu; val; ile; ala; tyr | leu |
| Pro (P) | ala | ala |
| Ser (S) | thr | thr |
| Thr (T) | ser | ser |
| Trp (W) | tyr; phe | tyr |
| Tyr (Y) | trp; phe; thr; ser | phe |
| Val (V) | ile; leu; met; phe; ala; norleucine | leu |

Substantial modifications in function or immunological identity of the PRO polypeptide are accomplished by selecting substitutions that differ significantly in their effect on maintaining (a) the structure of the polypeptide backbone in the area of the substitution, for example, as a sheet or helical conformation, (b) the charge or hydrophobicity of the molecule at the target site, or (c) the bulk of the side chain. Naturally occurring residues are divided into groups based on common side-chain properties:

(1) hydrophobic: norleucine, met, ala, val, leu, ile;

(2) neutral hydrophilic: cys, ser, thr;

(3) acidic: asp, glu;

(4) basic: asn, gln, his, lys, arg;

(5) residues that influence chain orientation: gly, pro; and

(6) aromatic: trp, tyr, phe.

Non-conservative substitutions will entail exchanging a member of one of these classes for another class. Such substituted residues also may be introduced into the conservative substitution sites or, more preferably, into the remaining (non-conserved) sites.

The variations can be made using methods known in the art such as oligonucleotide-mediated (site-directed) mutagenesis, alanine scanning, and PCR mutagenesis. Site-directed mutagenesis [Carter et al., Nucl. Acids Res., 13:4331 (1986); Zoller et al., Nucl. Acids Res., 10:6487 (1987)], cassette mutagenesis [Wells et al.,

Gene, 34:315 (1985)], restriction selection mutagenesis [Wells et al., Philos. Trans. R. Soc. London SerA, 317:415 (1986)] or other known techniques can be performed on the cloned DNA to produce the PRO variant DNA.

Scanning amino acid analysis can also be employed to identify one or more amino acids along a contiguous sequence. Among the preferred scanning amino acids are relatively small, neutral amino acids. Such amino acids include alanine, glycine, serine, and cysteine. Alanine is typically a preferred scanning amino acid among this group because it eliminates the side-chain beyond the beta-carbon and is less likely to alter the main-chain conformation of the variant [Cunningham and Wells, Science, 244: 1081-1085 (1989)]. Alanine is also typically preferred because it is the most common amino acid. Further, it is frequently found in both buried and exposed positions [Creighton, The Proteins, (W.H. Freeman & Co., N.Y.); Chothia, J. Mol. Biol., 150:1 (1976)]. If alanine substitution does not yield adequate amounts of variant, an isoteric amino acid can be used.

C. Modifications of PRO

Covalent modifications of PRO are included within the scope of this invention. One type of covalent modification includes reacting targeted amino acid residues of a PRO polypeptide with an organic derivatizing agent that is capable of reacting with selected side chains or the N- or C- terminal residues of the PRO. Derivatization with bifunctional agents is useful, for instance, for crosslinking PRO to a water-insoluble support matrix or surface for use in the method for purifying anti-PRO antibodies, and vice-versa. Commonly used crosslinking agents include, e.g., 1,1-bis(diazoacetyl)-2-phenylethane, glutaraldehyde, N-hydroxysuccinimide esters, for example, esters with 4-azidosalicylic acid, homobifunctional imidoesters, including disuccinimidyl esters such as 3,3'-dithiobis(succinimidylpropionate), bifunctional maleimides such as bis-N-maleimido-1,8-octane and agents such as methyl-3-[(p-azidophenyl)dithio]propioimidate.

Other modifications include deamidation of glutaminyl and asparaginyl residues to the corresponding glutamyl and aspartyl residues, respectively, hydroxylation of proline and lysine, phosphorylation of hydroxyl groups of seryl or threonyl residues, methylation of the α-amino groups of lysine, arginine, and histidine side chains [T.E. Creighton, Proteins: Structure and Molecular Properties, W.H. Freeman & Co., San Francisco, pp. 79-86 (1983)], acetylation of the N-terminal amine, and amidation of any C-terminal carboxyl group.

Another type of covalent modification of the PRO polypeptide included within the scope of this invention comprises altering the native glycosylation pattern of the polypeptide. "Altering the native glycosylation pattern" is intended for purposes herein to mean deleting one or more carbohydrate moieties found in native sequence PRO (either by removing the underlying glycosylation site or by deleting the glycosylation by chemical and/or enzymatic means), and/or adding one or more glycosylation sites that are not present in the native sequence PRO. In addition, the phrase includes qualitative changes in the glycosylation of the native proteins, involving a change in the nature and proportions of the various carbohydrate moieties present.

Addition of glycosylation sites to the PRO polypeptide may be accomplished by altering the amino acid sequence. The alteration may be made, for example, by the addition of, or substitution by, one or more serine or threonine residues to the native sequence PRO (for O-linked glycosylation sites). The PRO amino acid sequence may optionally be altered through changes at the DNA level, particularly by mutating the DNA encoding

the PRO polypeptide at preselected bases such that codons are generated that will translate into the desired amino acids.

Another means of increasing the number of carbohydrate moieties on the PRO polypeptide is by chemical or enzymatic coupling of glycosides to the polypeptide. Such methods are described in the art, e.g., in WO 87/05330 published 11 September 1987, and in Aplin and Wriston, CRC Crit. Rev. Biochem., pp. 259-306 (1981).

Removal of carbohydrate moieties present on the PRO polypeptide may be accomplished chemically or enzymatically or by mutational substitution of codons encoding for amino acid residues that serve as targets for glycosylation. Chemical deglycosylation techniques are known in the art and described, for instance, by Hakimuddin, et al., Arch. Biochem. Biophys., 259:52 (1987) and by Edge et al., Anal. Biochem., 118:131 (1981). Enzymatic cleavage of carbohydrate moieties on polypeptides can be achieved by the use of a variety of endo- and exo-glycosidases as described by Thotakura et al., Meth. Enzymol., 138:350 (1987).

Another type of covalent modification of PRO comprises linking the PRO polypeptide to one of a variety of nonproteinaceous polymers, e.g., polyethylene glycol (PEG), polypropylene glycol, or polyoxyalkylenes, in the manner set forth in U.S. Patent Nos. 4,640,835; 4,496,689; 4,301,144; 4,670,417; 4,791,192 or 4,179,337.

The PRO of the present invention may also be modified in a way to form a chimeric molecule comprising PRO fused to another, heterologous polypeptide or amino acid sequence.

In one embodiment, such a chimeric molecule comprises a fusion of the PRO with a tag polypeptide which provides an epitope to which an anti-tag antibody can selectively bind. The epitope tag is generally placed at the amino- or carboxyl- terminus of the PRO. The presence of such epitope-tagged forms of the PRO can be detected using an antibody against the tag polypeptide. Also, provision of the epitope tag enables the PRO to be readily purified by affinity purification using an anti-tag antibody or another type of affinity matrix that binds to the epitope tag. Various tag polypeptides and their respective antibodies are well known in the art. Examples include poly-histidine (poly-his) or poly-histidine-glycine (poly-his-gly) tags; the flu HA tag polypeptide and its antibody 12CA5 [Field et al., Mol. Cell. Biol., 8:2159-2165 (1988)]; the c-myc tag and the 8F9, 3C7, 6E10, G4, B7 and 9E10 antibodies thereto [Evan et al., Molecular and Cellular Biology, 5:3610-3616 (1985)]; and the Herpes Simplex virus glycoprotein D (gD) tag and its antibody [Paborsky et al., Protein Engineering, 3(6):547-553 (1990)]. Other tag polypeptides include the Flag-peptide [Hopp et al., BioTechnology, 6:1204-1210 (1988)]; the KT3 epitope peptide [Martin et al., Science, 255:192-194 (1992)]; an α-tubulin epitope peptide [Skinner et al., J. Biol. Chem., 266:15163-15166 (1991)]; and the T7 gene 10 protein peptide tag [Lutz-Freyermuth et al., Proc. Natl. Acad. Sci. USA, 87:6393-6397 (1990)].

In an alternative embodiment, the chimeric molecule may comprise a fusion of the PRO with an immunoglobulin or a particular region of an immunoglobulin. For a bivalent form of the chimeric molecule (also referred to as an "immunoadhesin"), such a fusion could be to the Fc region of an IgG molecule. The Ig fusions preferably include the substitution of a soluble (transmembrane domain deleted or inactivated) form of a PRO polypeptide in place of at least one variable region within an Ig molecule. In a particularly preferred embodiment, the immunoglobulin fusion includes the hinge, CH2 and CH3, or the hinge, CH1, CH2 and CH3 regions of an IgG1 molecule. For the production of immunoglobulin fusions see also US Patent No. 5,428,130 issued June 27,

1995.

D. Preparation of PRO

The description below relates primarily to production of PRO by culturing cells transformed or transfected with a vector containing PRO nucleic acid. It is, of course, contemplated that alternative methods, which are well known in the art, may be employed to prepare PRO. For instance, the PRO sequence, or portions thereof, may be produced by direct peptide synthesis using solid-phase techniques [see, e.g., Stewart et al., Solid-Phase Peptide Synthesis, W.H. Freeman Co., San Francisco, CA (1969); Merrifield, J. Am. Chem. Soc., 85:2149-2154 (1963)]. *In vitro* protein synthesis may be performed using manual techniques or by automation. Automated synthesis may be accomplished, for instance, using an Applied Biosystems Peptide Synthesizer (Foster City, CA) using manufacturer's instructions. Various portions of the PRO may be chemically synthesized separately and combined using chemical or enzymatic methods to produce the full-length PRO.

1. Isolation of DNA Encoding PRO

DNA encoding PRO may be obtained from a cDNA library prepared from tissue believed to possess the PRO mRNA and to express it at a detectable level. Accordingly, human PRO DNA can be conveniently obtained from a cDNA library prepared from human tissue, such as described in the Examples. The PRO-encoding gene may also be obtained from a genomic library or by known synthetic procedures (e.g., automated nucleic acid synthesis).

Libraries can be screened with probes (such as antibodies to the PRO or oligonucleotides of at least about 20-80 bases) designed to identify the gene of interest or the protein encoded by it. Screening the cDNA or genomic library with the selected probe may be conducted using standard procedures, such as described in Sambrook et al., Molecular Cloning: A Laboratory Manual (New York: Cold Spring Harbor Laboratory Press, 1989). An alternative means to isolate the gene encoding PRO is to use PCR methodology [Sambrook et al., supra; Dieffenbach et al., PCR Primer: A Laboratory Manual (Cold Spring Harbor Laboratory Press, 1995)].

The Examples below describe techniques for screening a cDNA library. The oligonucleotide sequences selected as probes should be of sufficient length and sufficiently unambiguous that false positives are minimized. The oligonucleotide is preferably labeled such that it can be detected upon hybridization to DNA in the library being screened. Methods of labeling are well known in the art, and include the use of radiolabels like $^{32}$P-labeled ATP, biotinylation or enzyme labeling. Hybridization conditions, including moderate stringency and high stringency, are provided in Sambrook et al., supra.

Sequences identified in such library screening methods can be compared and aligned to other known sequences deposited and available in public databases such as GenBank or other private sequence databases. Sequence identity (at either the amino acid or nucleotide level) within defined regions of the molecule or across the full-length sequence can be determined using methods known in the art and as described herein.

Nucleic acid having protein coding sequence may be obtained by screening selected cDNA or genomic libraries using the deduced amino acid sequence disclosed herein for the first time, and, if necessary, using conventional primer extension procedures as described in Sambrook et al., supra, to detect precursors and

processing intermediates of mRNA that may not have been reverse-transcribed into cDNA.

2. Selection and Transformation of Host Cells

Host cells are transfected or transformed with expression or cloning vectors described herein for PRO production and cultured in conventional nutrient media modified as appropriate for inducing promoters, selecting transformants, or amplifying the genes encoding the desired sequences. The culture conditions, such as media, temperature, pH and the like, can be selected by the skilled artisan without undue experimentation. In general, principles, protocols, and practical techniques for maximizing the productivity of cell cultures can be found in Mammalian Cell Biotechnology: a Practical Approach, M. Butler, ed. (IRL Press, 1991) and Sambrook et al., supra.

Methods of eukaryotic cell transfection and prokaryotic cell transformation are known to the ordinarily skilled artisan, for example, $CaCl_2$, $CaPO_4$, liposome-mediated and electroporation. Depending on the host cell used, transformation is performed using standard techniques appropriate to such cells. The calcium treatment employing calcium chloride, as described in Sambrook et al., supra, or electroporation is generally used for prokaryotes. Infection with *Agrobacterium tumefaciens* is used for transformation of certain plant cells, as described by Shaw et al., Gene, 23:315 (1983) and WO 89/05859 published 29 June 1989. For mammalian cells without such cell walls, the calcium phosphate precipitation method of Graham and van der Eb, Virology, 52:456-457 (1978) can be employed. General aspects of mammalian cell host system transfections have been described in U.S. Patent No. 4,399,216. Transformations into yeast are typically carried out according to the method of Van Solingen et al., J. Bact., 130:946 (1977) and Hsiao et al., Proc. Natl. Acad. Sci. (USA), 76:3829 (1979). However, other methods for introducing DNA into cells, such as by nuclear microinjection, electroporation, bacterial protoplast fusion with intact cells, or polycations, e.g., polybrene, polyornithine, may also be used. For various techniques for transforming mammalian cells, see Keown et al., Methods in Enzymology, 185:527-537 (1990) and Mansour et al., Nature, 336:348-352 (1988).

Suitable host cells for cloning or expressing the DNA in the vectors herein include prokaryote, yeast, or higher eukaryote cells. Suitable prokaryotes include but are not limited to eubacteria, such as Gram-negative or Gram-positive organisms, for example, Enterobacteriaceae such as *E. coli*. Various *E. coli* strains are publicly available, such as *E. coli* K12 strain MM294 (ATCC 31,446); *E. coli* X1776 (ATCC 31,537); *E. coli* strain W3110 (ATCC 27,325) and K5 772 (ATCC 53,635). Other suitable prokaryotic host cells include Enterobacteriaceae such as *Escherichia*, e.g., *E. coli*, *Enterobacter*, *Erwinia*, *Klebsiella*, *Proteus*, *Salmonella*, e.g., *Salmonella typhimurium*, *Serratia*, e.g., *Serratia marcescans*, and *Shigella*, as well as *Bacilli* such as *B. subtilis* and *B. licheniformis* (e.g., *B. licheniformis* 41P disclosed in DD 266,710 published 12 April 1989), *Pseudomonas* such as *P. aeruginosa*, and *Streptomyces*. These examples are illustrative rather than limiting. Strain W3110 is one particularly preferred host or parent host because it is a common host strain for recombinant DNA product fermentations. Preferably, the host cell secretes minimal amounts of proteolytic enzymes. For example, strain W3110 may be modified to effect a genetic mutation in the genes encoding proteins endogenous to the host, with examples of such hosts including *E. coli* W3110 strain 1A2, which has the complete genotype *tonA* ; *E. coli* W3110 strain 9E4, which has the complete genotype *tonA ptr3*; *E. coli* W3110 strain 27C7 (ATCC

55,244), which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT kan*r; *E. coli* W3110 strain 37D6, which has the complete genotype *tonA ptr3 phoA E15 (argF-lac)169 degP ompT rbs7 ilvG kan*r; *E. coli* W3110 strain 40B4, which is strain 37D6 with a non-kanamycin resistant *degP* deletion mutation; and an *E. coli* strain having mutant periplasmic protease disclosed in U.S. Patent No. 4,946,783 issued 7 August 1990. Alternatively, *in vitro* methods of cloning, e.g., PCR or other nucleic acid polymerase reactions, are suitable.

In addition to prokaryotes, eukaryotic microbes such as filamentous fungi or yeast are suitable cloning or expression hosts for PRO-encoding vectors. *Saccharomyces cerevisiae* is a commonly used lower eukaryotic host microorganism. Others include *Schizosaccharomyces pombe* (Beach and Nurse, Nature, 290: 140 [1981]; EP 139,383 published 2 May 1985); *Kluyveromyces* hosts (U.S. Patent No. 4,943,529; Fleer et al., Bio/Technology, 9:968-975 (1991)) such as, e.g., *K. lactis* (MW98-8C, CBS683, CBS4574; Louvencourt et al., J. Bacteriol., 154(2):737-742 [1983]), *K. fragilis* (ATCC 12,424), *K. bulgaricus* (ATCC 16,045), *K. wickeramii* (ATCC 24,178), *K. waltii* (ATCC 56,500), *K. drosophilarum* (ATCC 36,906; Van den Berg et al., Bio/Technology, 8:135 (1990)), *K. thermotolerans*, and *K. marxianus; yarrowia* (EP 402,226); *Pichia pastoris* (EP 183,070; Sreekrishna et al., J. Basic Microbiol., 28:265-278 [1988]); *Candida; Trichoderma reesia* (EP 244,234); *Neurospora crassa* (Case et al., Proc. Natl. Acad. Sci. USA, 76:5259-5263 [1979]); *Schwanniomyces* such as *Schwanniomyces occidentalis* (EP 394,538 published 31 October 1990); and filamentous fungi such as, e.g., *Neurospora, Penicillium, Tolypocladium* (WO 91/00357 published 10 January 1991), and *Aspergillus* hosts such as *A. nidulans* (Ballance et al., Biochem. Biophys. Res. Commun., 112:284-289 [1983]; Tilburn et al., Gene, 26:205-221 [1983]; Yelton et al., Proc. Natl. Acad. Sci. USA, 81: 1470-1474 [1984]) and *A. niger* (Kelly and Hynes, EMBO J., 4:475-479 [1985]). Methylotropic yeasts are suitable herein and include, but are not limited to, yeast capable of growth on methanol selected from the genera consisting of *Hansenula, Candida, Kloeckera, Pichia, Saccharomyces, Torulopsis,* and *Rhodotorula*. A list of specific species that are exemplary of this class of yeasts may be found in C. Anthony, The Biochemistry of Methylotrophs, 269 (1982).

Suitable host cells for the expression of glycosylated PRO are derived from multicellular organisms. Examples of invertebrate cells include insect cells such as Drosophila S2 and Spodoptera Sf9, as well as plant cells. Examples of useful mammalian host cell lines include Chinese hamster ovary (CHO) and COS cells. More specific examples include monkey kidney CV1 line transformed by SV40 (COS-7, ATCC CRL 1651); human embryonic kidney line (293 or 293 cells subcloned for growth in suspension culture, Graham et al., J. Gen Virol., 36:59 (1977)); Chinese hamster ovary cells/-DHFR (CHO, Urlaub and Chasin, Proc. Natl. Acad. Sci. USA, 77:4216 (1980)); mouse sertoli cells (TM4, Mather, Biol. Reprod., 23:243-251 (1980)); human lung cells (W138, ATCC CCL 75); human liver cells (Hep G2, HB 8065); and mouse mammary tumor (MMT 060562, ATCC CCL51). The selection of the appropriate host cell is deemed to be within the skill in the art.

### 3. Selection and Use of a Replicable Vector

The nucleic acid (e.g., cDNA or genomic DNA) encoding PRO may be inserted into a replicable vector for cloning (amplification of the DNA) or for expression. Various vectors are publicly available. The vector may, for example, be in the form of a plasmid, cosmid, viral particle, or phage. The appropriate nucleic acid sequence may be inserted into the vector by a variety of procedures. In general, DNA is inserted into an

appropriate restriction endonuclease site(s) using techniques known in the art. Vector components generally include, but are not limited to, one or more of a signal sequence, an origin of replication, one or more marker genes, an enhancer element, a promoter, and a transcription termination sequence. Construction of suitable vectors containing one or more of these components employs standard ligation techniques which are known to the skilled artisan.

The PRO may be produced recombinantly not only directly, but also as a fusion polypeptide with a heterologous polypeptide, which may be a signal sequence or other polypeptide having a specific cleavage site at the N-terminus of the mature protein or polypeptide. In general, the signal sequence may be a component of the vector, or it may be a part of the PRO-encoding DNA that is inserted into the vector. The signal sequence may be a prokaryotic signal sequence selected, for example, from the group of the alkaline phosphatase, penicillinase, lpp, or heat-stable enterotoxin II leaders. For yeast secretion the signal sequence may be, e.g., the yeast invertase leader, alpha factor leader (including *Saccharomyces* and *Kluyveromyces* α-factor leaders, the latter described in U.S. Patent No. 5,010,182), or acid phosphatase leader, the *C. albicans* glucoamylase leader (EP 362,179 published 4 April 1990), or the signal described in WO 90/13646 published 15 November 1990. In mammalian cell expression, mammalian signal sequences may be used to direct secretion of the protein, such as signal sequences from secreted polypeptides of the same or related species, as well as viral secretory leaders.

Both expression and cloning vectors contain a nucleic acid sequence that enables the vector to replicate in one or more selected host cells. Such sequences are well known for a variety of bacteria, yeast, and viruses. The origin of replication from the plasmid pBR322 is suitable for most Gram-negative bacteria, the 2μ plasmid origin is suitable for yeast, and various viral origins (SV40, polyoma, adenovirus, VSV or BPV) are useful for cloning vectors in mammalian cells.

Expression and cloning vectors will typically contain a selection gene, also termed a selectable marker. Typical selection genes encode proteins that (a) confer resistance to antibiotics or other toxins, e.g., ampicillin, neomycin, methotrexate, or tetracycline, (b) complement auxotrophic deficiencies, or (c) supply critical nutrients not available from complex media, e.g., the gene encoding D-alanine racemase for *Bacilli*.

An example of suitable selectable markers for mammalian cells are those that enable the identification of cells competent to take up the PRO-encoding nucleic acid, such as DHFR or thymidine kinase. An appropriate host cell when wild-type DHFR is employed is the CHO cell line deficient in DHFR activity, prepared and propagated as described by Urlaub et al., Proc. Natl. Acad. Sci. USA, 77:4216 (1980). A suitable selection gene for use in yeast is the *trp*1 gene present in the yeast plasmid YRp7 [Stinchcomb et al., Nature, 282:39 (1979); Kingsman et al., Gene, 7:141 (1979); Tschemper et al., Gene, 10:157 (1980)]. The *trp*1 gene provides a selection marker for a mutant strain of yeast lacking the ability to grow in tryptophan, for example, ATCC No. 44076 or PEP4-1 [Jones, Genetics, 85:12 (1977)].

Expression and cloning vectors usually contain a promoter operably linked to the PRO-encoding nucleic acid sequence to direct mRNA synthesis. Promoters recognized by a variety of potential host cells are well known. Promoters suitable for use with prokaryotic hosts include the β-lactamase and lactose promoter systems [Chang et al., Nature, 275:615 (1978); Goeddel et al., Nature, 281:544 (1979)], alkaline phosphatase, a tryptophan (trp) promoter system [Goeddel, Nucleic Acids Res., 8:4057 (1980); EP 36,776], and hybrid

promoters such as the tac promoter [deBoer et al., Proc. Natl. Acad. Sci. USA, 80:21-25 (1983)]. Promoters for use in bacterial systems also will contain a Shine-Dalgarno (S.D.) sequence operably linked to the DNA encoding PRO.

Examples of suitable promoting sequences for use with yeast hosts include the promoters for 3-phosphoglycerate kinase [Hitzeman et al., J. Biol. Chem., 255:2073 (1980)] or other glycolytic enzymes [Hess et al., J. Adv. Enzyme Reg., 7:149 (1968); Holland, Biochemistry, 17:4900 (1978)], such as enolase, glyceraldehyde-3-phosphate dehydrogenase, hexokinase, pyruvate decarboxylase, phosphofructokinase, glucose-6-phosphate isomerase, 3-phosphoglycerate mutase, pyruvate kinase, triosephosphate isomerase, phosphoglucose isomerase, and glucokinase.

Other yeast promoters, which are inducible promoters having the additional advantage of transcription controlled by growth conditions, are the promoter regions for alcohol dehydrogenase 2, isocytochrome C, acid phosphatase, degradative enzymes associated with nitrogen metabolism, metallothionein, glyceraldehyde-3-phosphate dehydrogenase, and enzymes responsible for maltose and galactose utilization. Suitable vectors and promoters for use in yeast expression are further described in EP 73,657.

PRO transcription from vectors in mammalian host cells is controlled, for example, by promoters obtained from the genomes of viruses such as polyoma virus, fowlpox virus (UK 2,211,504 published 5 July 1989), adenovirus (such as Adenovirus 2), bovine papilloma virus, avian sarcoma virus, cytomegalovirus, a retrovirus, hepatitis-B virus and Simian Virus 40 (SV40), from heterologous mammalian promoters, e.g., the actin promoter or an immunoglobulin promoter, and from heat-shock promoters, provided such promoters are compatible with the host cell systems.

Transcription of a DNA encoding the PRO by higher eukaryotes may be increased by inserting an enhancer sequence into the vector. Enhancers are cis-acting elements of DNA, usually about from 10 to 300 bp, that act on a promoter to increase its transcription. Many enhancer sequences are now known from mammalian genes (globin, elastase, albumin, α-fetoprotein, and insulin). Typically, however, one will use an enhancer from a eukaryotic cell virus. Examples include the SV40 enhancer on the late side of the replication origin (bp 100-270), the cytomegalovirus early promoter enhancer, the polyoma enhancer on the late side of the replication origin, and adenovirus enhancers. The enhancer may be spliced into the vector at a position 5' or 3' to the PRO coding sequence, but is preferably located at a site 5' from the promoter.

Expression vectors used in eukaryotic host cells (yeast, fungi, insect, plant, animal, human, or nucleated cells from other multicellular organisms) will also contain sequences necessary for the termination of transcription and for stabilizing the mRNA. Such sequences are commonly available from the 5' and, occasionally 3', untranslated regions of eukaryotic or viral DNAs or cDNAs. These regions contain nucleotide segments transcribed as polyadenylated fragments in the untranslated portion of the mRNA encoding PRO.

Still other methods, vectors, and host cells suitable for adaptation to the synthesis of PRO in recombinant vertebrate cell culture are described in Gething et al., Nature, 293:620-625 (1981); Mantei et al., Nature, 281:40-46 (1979); EP 117,060; and EP 117,058.

4. Detecting Gene Amplification/Expression

Gene amplification and/or expression may be measured in a sample directly, for example, by conventional Southern blotting, Northern blotting to quantitate the transcription of mRNA [Thomas, Proc. Natl. Acad. Sci. USA, 77:5201-5205 (1980)], dot blotting (DNA analysis), or *in situ* hybridization, using an appropriately labeled probe, based on the sequences provided herein. Alternatively, antibodies may be employed that can recognize specific duplexes, including DNA duplexes, RNA duplexes, and DNA-RNA hybrid duplexes or DNA-protein duplexes. The antibodies in turn may be labeled and the assay may be carried out where the duplex is bound to a surface, so that upon the formation of duplex on the surface, the presence of antibody bound to the duplex can be detected.

Gene expression, alternatively, may be measured by immunological methods, such as immunohistochemical staining of cells or tissue sections and assay of cell culture or body fluids, to quantitate directly the expression of gene product. Antibodies useful for immunohistochemical staining and/or assay of sample fluids may be either monoclonal or polyclonal, and may be prepared in any mammal. Conveniently, the antibodies may be prepared against a native sequence PRO polypeptide or against a synthetic peptide based on the DNA sequences provided herein or against exogenous sequence fused to PRO DNA and encoding a specific antibody epitope.

5. Purification of Polypeptide

Forms of PRO may be recovered from culture medium or from host cell lysates. If membrane-bound, it can be released from the membrane using a suitable detergent solution (e.g. Triton-X 100) or by enzymatic cleavage. Cells employed in expression of PRO can be disrupted by various physical or chemical means, such as freeze-thaw cycling, sonication, mechanical disruption, or cell lysing agents.

It may be desired to purify PRO from recombinant cell proteins or polypeptides. The following procedures are exemplary of suitable purification procedures: by fractionation on an ion-exchange column; ethanol precipitation; reverse phase HPLC; chromatography on silica or on a cation-exchange resin such as DEAE; chromatofocusing; SDS-PAGE; ammonium sulfate precipitation; gel filtration using, for example, Sephadex G-75; protein A Sepharose columns to remove contaminants such as IgG; and metal chelating columns to bind epitope-tagged forms of the PRO. Various methods of protein purification may be employed and such methods are known in the art and described for example in Deutscher, Methods in Enzymology, 182 (1990); Scopes, Protein Purification: Principles and Practice, Springer-Verlag, New York (1982). The purification step(s) selected will depend, for example, on the nature of the production process used and the particular PRO produced.

E. Uses for PRO

Nucleotide sequences (or their complement) encoding PRO have various applications in the art of molecular biology, including uses as hybridization probes, in chromosome and gene mapping and in the generation of anti-sense RNA and DNA. PRO nucleic acid will also be useful for the preparation of PRO polypeptides by the recombinant techniques described herein.

The full-length native sequence PRO gene, or portions thereof, may be used as hybridization probes for

a cDNA library to isolate the full-length PRO cDNA or to isolate still other cDNAs (for instance, those encoding naturally-occurring variants of PRO or PRO from other species) which have a desired sequence identity to the native PRO sequence disclosed herein. Optionally, the length of the probes will be about 20 to about 50 bases. The hybridization probes may be derived from at least partially novel regions of the full length native nucleotide sequence wherein those regions may be determined without undue experimentation or from genomic sequences including promoters, enhancer elements and introns of native sequence PRO. By way of example, a screening method will comprise isolating the coding region of the PRO gene using the known DNA sequence to synthesize a selected probe of about 40 bases. Hybridization probes may be labeled by a variety of labels, including radionucleotides such as $^{32}P$ or $^{35}S$, or enzymatic labels such as alkaline phosphatase coupled to the probe via avidin/biotin coupling systems. Labeled probes having a sequence complementary to that of the PRO gene of the present invention can be used to screen libraries of human cDNA, genomic DNA or mRNA to determine which members of such libraries the probe hybridizes to. Hybridization techniques are described in further detail in the Examples below.

Any EST sequences disclosed in the present application may similarly be employed as probes, using the methods disclosed herein.

Other useful fragments of the PRO nucleic acids include antisense or sense oligonucleotides comprising a singe-stranded nucleic acid sequence (either RNA or DNA) capable of binding to target PRO mRNA (sense) or PRO DNA (antisense) sequences. Antisense or sense oligonucleotides, according to the present invention, comprise a fragment of the coding region of PRO DNA. Such a fragment generally comprises at least about 14 nucleotides, preferably from about 14 to 30 nucleotides. The ability to derive an antisense or a sense oligonucleotide, based upon a cDNA sequence encoding a given protein is described in, for example, Stein and Cohen (Cancer Res. 48:2659, 1988) and van der Krol et al. (BioTechniques 6:958, 1988).

Binding of antisense or sense oligonucleotides to target nucleic acid sequences results in the formation of duplexes that block transcription or translation of the target sequence by one of several means, including enhanced degradation of the duplexes, premature termination of transcription or translation, or by other means. The antisense oligonucleotides thus may be used to block expression of PRO proteins. Antisense or sense oligonucleotides further comprise oligonucleotides having modified sugar-phosphodiester backbones (or other sugar linkages, such as those described in WO 91/06629) and wherein such sugar linkages are resistant to endogenous nucleases. Such oligonucleotides with resistant sugar linkages are stable *in vivo* (i.e., capable of resisting enzymatic degradation) but retain sequence specificity to be able to bind to target nucleotide sequences.

Other examples of sense or antisense oligonucleotides include those oligonucleotides which are covalently linked to organic moieties, such as those described in WO 90/10048, and other moieties that increases affinity of the oligonucleotide for a target nucleic acid sequence, such as poly-(L-lysine). Further still, intercalating agents, such as ellipticine, and alkylating agents or metal complexes may be attached to sense or antisense oligonucleotides to modify binding specificities of the antisense or sense oligonucleotide for the target nucleotide sequence.

Antisense or sense oligonucleotides may be introduced into a cell containing the target nucleic acid sequence by any gene transfer method, including, for example, $CaPO_4$-mediated DNA transfection,

electroporation, or by using gene transfer vectors such as Epstein-Barr virus. In a preferred procedure, an antisense or sense oligonucleotide is inserted into a suitable retroviral vector. A cell containing the target nucleic acid sequence is contacted with the recombinant retroviral vector, either *in vivo* or *ex vivo*. Suitable retroviral vectors include, but are not limited to, those derived from the murine retrovirus M-MuLV, N2 (a retrovirus derived from M-MuLV), or the double copy vectors designated DCT5A, DCT5B and DCT5C (see WO 90/13641).

Sense or antisense oligonucleotides also may be introduced into a cell containing the target nucleotide sequence by formation of a conjugate with a ligand binding molecule, as described in WO 91/04753. Suitable ligand binding molecules include, but are not limited to, cell surface receptors, growth factors, other cytokines, or other ligands that bind to cell surface receptors. Preferably, conjugation of the ligand binding molecule does not substantially interfere with the ability of the ligand binding molecule to bind to its corresponding molecule or receptor, or block entry of the sense or antisense oligonucleotide or its conjugated version into the cell.

Alternatively, a sense or an antisense oligonucleotide may be introduced into a cell containing the target nucleic acid sequence by formation of an oligonucleotide-lipid complex, as described in WO 90/10448. The sense or antisense oligonucleotide-lipid complex is preferably dissociated within the cell by an endogenous lipase.

Antisense or sense RNA or DNA molecules are generally at least about 5 bases in length, about 10 bases in length, about 15 bases in length, about 20 bases in length, about 25 bases in length, about 30 bases in length, about 35 bases in length, about 40 bases in length, about 45 bases in length, about 50 bases in length, about 55 bases in length, about 60 bases in length, about 65 bases in length, about 70 bases in length, about 75 bases in length, about 80 bases in length, about 85 bases in length, about 90 bases in length, about 95 bases in length, about 100 bases in length, or more.

The probes may also be employed in PCR techniques to generate a pool of sequences for identification of closely related PRO coding sequences.

Nucleotide sequences encoding a PRO can also be used to construct hybridization probes for mapping the gene which encodes that PRO and for the genetic analysis of individuals with genetic disorders. The nucleotide sequences provided herein may be mapped to a chromosome and specific regions of a chromosome using known techniques, such as *in situ* hybridization, linkage analysis against known chromosomal markers, and hybridization screening with libraries.

When the coding sequences for PRO encode a protein which binds to another protein (example, where the PRO is a receptor), the PRO can be used in assays to identify the other proteins or molecules involved in the binding interaction. By such methods, inhibitors of the receptor/ligand binding interaction can be identified. Proteins involved in such binding interactions can also be used to screen for peptide or small molecule inhibitors or agonists of the binding interaction. Also, the receptor PRO can be used to isolate correlative ligand(s). Screening assays can be designed to find lead compounds that mimic the biological activity of a native PRO or a receptor for PRO. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates. Small molecules contemplated include synthetic organic or inorganic compounds. The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays and cell based

assays, which are well characterized in the art.

Nucleic acids which encode PRO or its modified forms can also be used to generate either transgenic animals or "knock out" animals which, in turn, are useful in the development and screening of therapeutically useful reagents. A transgenic animal (e.g., a mouse or rat) is an animal having cells that contain a transgene, which transgene was introduced into the animal or an ancestor of the animal at a prenatal, e.g., an embryonic stage. A transgene is a DNA which is integrated into the genome of a cell from which a transgenic animal develops. In one embodiment, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques and the genomic sequences used to generate transgenic animals that contain cells which express DNA encoding PRO. Methods for generating transgenic animals, particularly animals such as mice or rats, have become conventional in the art and are described, for example, in U.S. Patent Nos. 4,736,866 and 4,870,009. Typically, particular cells would be targeted for PRO transgene incorporation with tissue-specific enhancers. Transgenic animals that include a copy of a transgene encoding PRO introduced into the germ line of the animal at an embryonic stage can be used to examine the effect of increased expression of DNA encoding PRO. Such animals can be used as tester animals for reagents thought to confer protection from, for example, pathological conditions associated with its overexpression. In accordance with this facet of the invention, an animal is treated with the reagent and a reduced incidence of the pathological condition, compared to untreated animals bearing the transgene, would indicate a potential therapeutic intervention for the pathological condition.

Alternatively, non-human homologues of PRO can be used to construct a PRO "knock out" animal which has a defective or altered gene encoding PRO as a result of homologous recombination between the endogenous gene encoding PRO and altered genomic DNA encoding PRO introduced into an embryonic stem cell of the animal. For example, cDNA encoding PRO can be used to clone genomic DNA encoding PRO in accordance with established techniques. A portion of the genomic DNA encoding PRO can be deleted or replaced with another gene, such as a gene encoding a selectable marker which can be used to monitor integration. Typically, several kilobases of unaltered flanking DNA (both at the 5' and 3' ends) are included in the vector [see e.g., Thomas and Capecchi, Cell, 51:503 (1987) for a description of homologous recombination vectors]. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced DNA has homologously recombined with the endogenous DNA are selected [see e.g., Li et al., Cell, 69:915 (1992)]. The selected cells are then injected into a blastocyst of an animal (e.g., a mouse or rat) to form aggregation chimeras [see e.g., Bradley, in *Teratocarcinomas and Embryonic Stem Cells: A Practical Approach*, E. J. Robertson, ed. (IRL, Oxford, 1987), pp. 113-152]. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term to create a "knock out" animal. Progeny harboring the homologously recombined DNA in their germ cells can be identified by standard techniques and used to breed animals in which all cells of the animal contain the homologously recombined DNA. Knockout animals can be characterized for instance, for their ability to defend against certain pathological conditions and for their development of pathological conditions due to absence of the PRO polypeptide.

Nucleic acid encoding the PRO polypeptides may also be used in gene therapy. In gene therapy applications, genes are introduced into cells in order to achieve *in vivo* synthesis of a therapeutically effective

genetic product, for example for replacement of a defective gene. "Gene therapy" includes both conventional gene therapy where a lasting effect is achieved by a single treatment, and the administration of gene therapeutic agents, which involves the one time or repeated administration of a therapeutically effective DNA or mRNA. Antisense RNAs and DNAs can be used as therapeutic agents for blocking the expression of certain genes *in vivo*. It has already been shown that short antisense oligonucleotides can be imported into cells where they act as inhibitors, despite their low intracellular concentrations caused by their restricted uptake by the cell membrane. (Zamecnik *et al.*, Proc. Natl. Acad. Sci. USA 83:4143-4146 [1986]). The oligonucleotides can be modified to enhance their uptake, e.g. by substituting their negatively charged phosphodiester groups by uncharged groups.

There are a variety of techniques available for introducing nucleic acids into viable cells. The techniques vary depending upon whether the nucleic acid is transferred into cultured cells *in vitro*, or *in vivo* in the cells of the intended host. Techniques suitable for the transfer of nucleic acid into mammalian cells *in vitro* include the use of liposomes, electroporation, microinjection, cell fusion, DEAE-dextran, the calcium phosphate precipitation method, etc. The currently preferred *in vivo* gene transfer techniques include transfection with viral (typically retroviral) vectors and viral coat protein-liposome mediated transfection (Dzau et al., Trends in Biotechnology 11, 205-210 [1993]). In some situations it is desirable to provide the nucleic acid source with an agent that targets the target cells, such as an antibody specific for a cell surface membrane protein or the target cell, a ligand for a receptor on the target cell, etc. Where liposomes are employed, proteins which bind to a cell surface membrane protein associated with endocytosis may be used for targeting and/or to facilitate uptake, e.g. capsid proteins or fragments thereof tropic for a particular cell type, antibodies for proteins which undergo internalization in cycling, proteins that target intracellular localization and enhance intracellular half-life. The technique of receptor-mediated endocytosis is described, for example, by Wu et al., J. Biol. Chem. 262, 4429-4432 (1987); and Wagner et al., Proc. Natl. Acad. Sci. USA 87, 3410-3414 (1990). For review of gene marking and gene therapy protocols see Anderson et al., Science 256, 808-813 (1992).

The PRO polypeptides described herein may also be employed as molecular weight markers for protein electrophoresis purposes and the isolated nucleic acid sequences may be used for recombinantly expressing those markers.

The nucleic acid molecules encoding the PRO polypeptides or fragments thereof described herein are useful for chromosome identification. In this regard, there exists an ongoing need to identify new chromosome markers, since relatively few chromosome marking reagents, based upon actual sequence data are presently available. Each PRO nucleic acid molecule of the present invention can be used as a chromosome marker.

The PRO polypeptides and nucleic acid molecules of the present invention may also be used diagnostically for tissue typing, wherein the PRO polypeptides of the present invention may be differentially expressed in one tissue as compared to another, preferably in a diseased tissue as compared to a normal tissue of the same tissue type. PRO nucleic acid molecules will find use for generating probes for PCR, Northern analysis, Southern analysis and Western analysis.

The PRO polypeptides described herein may also be employed as therapeutic agents. The PRO polypeptides of the present invention can be formulated according to known methods to prepare pharmaceutically useful compositions, whereby the PRO product hereof is combined in admixture with a pharmaceutically

acceptable carrier vehicle. Therapeutic formulations are prepared for storage by mixing the active ingredient having the desired degree of purity with optional physiologically acceptable carriers, excipients or stabilizers (Remington's Pharmaceutical Sciences 16th edition, Osol, A. Ed. (1980)), in the form of lyophilized formulations or aqueous solutions. Acceptable carriers, excipients or stabilizers are nontoxic to recipients at the dosages and concentrations employed, and include buffers such as phosphate, citrate and other organic acids; antioxidants including ascorbic acid; low molecular weight (less than about 10 residues) polypeptides; proteins, such as serum albumin, gelatin or immunoglobulins; hydrophilic polymers such as polyvinylpyrrolidone, amino acids such as glycine, glutamine, asparagine, arginine or lysine; monosaccharides, disaccharides and other carbohydrates including glucose, mannose, or dextrins; chelating agents such as EDTA; sugar alcohols such as mannitol or sorbitol; salt-forming counterions such as sodium; and/or nonionic surfactants such as TWEEN™, PLURONICS™ or PEG.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes, prior to or following lyophilization and reconstitution.

Therapeutic compositions herein generally are placed into a container having a sterile access port, for example, an intravenous solution bag or vial having a stopper pierceable by a hypodermic injection needle.

The route of administration is in accord with known methods, e.g. injection or infusion by intravenous, intraperitoneal, intracerebral, intramuscular, intraocular, intraarterial or intralesional routes, topical administration, or by sustained release systems.

Dosages and desired drug concentrations of pharmaceutical compositions of the present invention may vary depending on the particular use envisioned. The determination of the appropriate dosage or route of administration is well within the skill of an ordinary physician. Animal experiments provide reliable guidance for the determination of effective doses for human therapy. Interspecies scaling of effective doses can be performed following the principles laid down by Mordenti, J. and Chappell, W. "The use of interspecies scaling in toxicokinetics" In Toxicokinetics and New Drug Development, Yacobi et al., Eds., Pergamon Press, New York 1989, pp. 42-96.

When *in vivo* administration of a PRO polypeptide or agonist or antagonist thereof is employed, normal dosage amounts may vary from about 10 ng/kg to up to 100 mg/kg of mammal body weight or more per day, preferably about 1 μg/kg/day to 10 mg/kg/day, depending upon the route of administration. Guidance as to particular dosages and methods of delivery is provided in the literature; see, for example, U.S. Pat. Nos. 4,657,760; 5,206,344; or 5,225,212. It is anticipated that different formulations will be effective for different treatment compounds and different disorders, that administration targeting one organ or tissue, for example, may necessitate delivery in a manner different from that to another organ or tissue.

Where sustained-release administration of a PRO polypeptide is desired in a formulation with release characteristics suitable for the treatment of any disease or disorder requiring administration of the PRO polypeptide, microencapsulation of the PRO polypeptide is contemplated. Microencapsulation of recombinant proteins for sustained release has been successfully performed with human growth hormone (rhGH), interferon-(rhIFN- ), interleukin-2, and MN rgp120. Johnson et al., Nat. Med., 2:795-799 (1996); Yasuda, Biomed. Ther., 27:1221-1223 (1993); Hora et al., Bio/Technology, 8:755-758 (1990); Cleland, "Design and Production of Single

Immunization Vaccines Using Polylactide Polyglycolide Microsphere Systems," in Vaccine Design: The Subunit and Adjuvant Approach, Powell and Newman, eds, (Plenum Press: New York, 1995), pp. 439-462; WO 97/03692, WO 96/40072, WO 96/07399; and U.S. Pat. No. 5,654,010.

The sustained-release formulations of these proteins were developed using poly-lactic-coglycolic acid (PLGA) polymer due to its biocompatibility and wide range of biodegradable properties. The degradation products of PLGA, lactic and glycolic acids, can be cleared quickly within the human body. Moreover, the degradability of this polymer can be adjusted from months to years depending on its molecular weight and composition. Lewis, "Controlled release of bioactive agents from lactide/glycolide polymer," in: M. Chasin and R. Langer (Eds.), Biodegradable Polymers as Drug Delivery Systems (Marcel Dekker: New York, 1990), pp. 1-41.

This invention encompasses methods of screening compounds to identify those that mimic the PRO polypeptide (agonists) or prevent the effect of the PRO polypeptide (antagonists). Screening assays for antagonist drug candidates are designed to identify compounds that bind or complex with the PRO polypeptides encoded by the genes identified herein, or otherwise interfere with the interaction of the encoded polypeptides with other cellular proteins. Such screening assays will include assays amenable to high-throughput screening of chemical libraries, making them particularly suitable for identifying small molecule drug candidates.

The assays can be performed in a variety of formats, including protein-protein binding assays, biochemical screening assays, immunoassays, and cell-based assays, which are well characterized in the art.

All assays for antagonists are common in that they call for contacting the drug candidate with a PRO polypeptide encoded by a nucleic acid identified herein under conditions and for a time sufficient to allow these two components to interact.

In binding assays, the interaction is binding and the complex formed can be isolated or detected in the reaction mixture. In a particular embodiment, the PRO polypeptide encoded by the gene identified herein or the drug candidate is immobilized on a solid phase, e.g., on a microtiter plate, by covalent or non-covalent attachments. Non-covalent attachment generally is accomplished by coating the solid surface with a solution of the PRO polypeptide and drying. Alternatively, an immobilized antibody, e.g., a monoclonal antibody, specific for the PRO polypeptide to be immobilized can be used to anchor it to a solid surface. The assay is performed by adding the non-immobilized component, which may be labeled by a detectable label, to the immobilized component, e.g., the coated surface containing the anchored component. When the reaction is complete, the non-reacted components are removed, e.g., by washing, and complexes anchored on the solid surface are detected. When the originally non-immobilized component carries a detectable label, the detection of label immobilized on the surface indicates that complexing occurred. Where the originally non-immobilized component does not carry a label, complexing can be detected, for example, by using a labeled antibody specifically binding the immobilized complex.

If the candidate compound interacts with but does not bind to a particular PRO polypeptide encoded by a gene identified herein, its interaction with that polypeptide can be assayed by methods well known for detecting protein-protein interactions. Such assays include traditional approaches, such as, e.g., cross-linking, co-immunoprecipitation, and co-purification through gradients or chromatographic columns. In addition, protein-protein interactions can be monitored by using a yeast-based genetic system described by Fields and co-workers

(Fields and Song, Nature (London), 340:245-246 (1989); Chien et al., Proc. Natl. Acad. Sci. USA, 88:9578-9582 (1991)) as disclosed by Chevray and Nathans, Proc. Natl. Acad. Sci. USA, 89: 5789-5793 (1991). Many transcriptional activators, such as yeast GAL4, consist of two physically discrete modular domains, one acting as the DNA-binding domain, the other one functioning as the transcription-activation domain. The yeast expression system described in the foregoing publications (generally referred to as the "two-hybrid system") takes advantage of this property, and employs two hybrid proteins, one in which the target protein is fused to the DNA-binding domain of GAL4, and another, in which candidate activating proteins are fused to the activation domain. The expression of a GAL1-*lacZ* reporter gene under control of a GAL4-activated promoter depends on reconstitution of GAL4 activity via protein-protein interaction. Colonies containing interacting polypeptides are detected with a chromogenic substrate for β-galactosidase. A complete kit (MATCHMAKER™) for identifying protein-protein interactions between two specific proteins using the two-hybrid technique is commercially available from Clontech. This system can also be extended to map protein domains involved in specific protein interactions as well as to pinpoint amino acid residues that are crucial for these interactions.

Compounds that interfere with the interaction of a gene encoding a PRO polypeptide identified herein and other intra- or extracellular components can be tested as follows: usually a reaction mixture is prepared containing the product of the gene and the intra- or extracellular component under conditions and for a time allowing for the interaction and binding of the two products. To test the ability of a candidate compound to inhibit binding, the reaction is run in the absence and in the presence of the test compound. In addition, a placebo may be added to a third reaction mixture, to serve as positive control. The binding (complex formation) between the test compound and the intra- or extracellular component present in the mixture is monitored as described hereinabove. The formation of a complex in the control reaction(s) but not in the reaction mixture containing the test compound indicates that the test compound interferes with the interaction of the test compound and its reaction partner.

To assay for antagonists, the PRO polypeptide may be added to a cell along with the compound to be screened for a particular activity and the ability of the compound to inhibit the activity of interest in the presence of the PRO polypeptide indicates that the compound is an antagonist to the PRO polypeptide. Alternatively, antagonists may be detected by combining the PRO polypeptide and a potential antagonist with membrane-bound PRO polypeptide receptors or recombinant receptors under appropriate conditions for a competitive inhibition assay. The PRO polypeptide can be labeled, such as by radioactivity, such that the number of PRO polypeptide molecules bound to the receptor can be used to determine the effectiveness of the potential antagonist. The gene encoding the receptor can be identified by numerous methods known to those of skill in the art, for example, ligand panning and FACS sorting. Coligan et al., Current Protocols in Immun., 1(2): Chapter 5 (1991). Preferably, expression cloning is employed wherein polyadenylated RNA is prepared from a cell responsive to the PRO polypeptide and a cDNA library created from this RNA is divided into pools and used to transfect COS cells or other cells that are not responsive to the PRO polypeptide. Transfected cells that are grown on glass slides are exposed to labeled PRO polypeptide. The PRO polypeptide can be labeled by a variety of means including iodination or inclusion of a recognition site for a site-specific protein kinase. Following fixation and incubation, the slides are subjected to autoradiographic analysis. Positive pools are identified and sub-pools are

prepared and re-transfected using an interactive sub-pooling and re-screening process, eventually yielding a single clone that encodes the putative receptor.

As an alternative approach for receptor identification, labeled PRO polypeptide can be photoaffinity-linked with cell membrane or extract preparations that express the receptor molecule. Cross-linked material is resolved by PAGE and exposed to X-ray film. The labeled complex containing the receptor can be excised, resolved into peptide fragments, and subjected to protein micro-sequencing. The amino acid sequence obtained from micro- sequencing would be used to design a set of degenerate oligonucleotide probes to screen a cDNA library to identify the gene encoding the putative receptor.

In another assay for antagonists, mammalian cells or a membrane preparation expressing the receptor would be incubated with labeled PRO polypeptide in the presence of the candidate compound. The ability of the compound to enhance or block this interaction could then be measured.

More specific examples of potential antagonists include an oligonucleotide that binds to the fusions of immunoglobulin with PRO polypeptide, and, in particular, antibodies including, without limitation, poly- and monoclonal antibodies and antibody fragments, single-chain antibodies, anti-idiotypic antibodies, and chimeric or humanized versions of such antibodies or fragments, as well as human antibodies and antibody fragments. Alternatively, a potential antagonist may be a closely related protein, for example, a mutated form of the PRO polypeptide that recognizes the receptor but imparts no effect, thereby competitively inhibiting the action of the PRO polypeptide.

Another potential PRO polypeptide antagonist is an antisense RNA or DNA construct prepared using antisense technology, where, e.g., an antisense RNA or DNA molecule acts to block directly the translation of mRNA by hybridizing to targeted mRNA and preventing protein translation. Antisense technology can be used to control gene expression through triple-helix formation or antisense DNA or RNA, both of which methods are based on binding of a polynucleotide to DNA or RNA. For example, the 5' coding portion of the polynucleotide sequence, which encodes the mature PRO polypeptides herein, is used to design an antisense RNA oligonucleotide of from about 10 to 40 base pairs in length. A DNA oligonucleotide is designed to be complementary to a region of the gene involved in transcription (triple helix - see Lee et al., Nucl. Acids Res., 6:3073 (1979); Cooney et al., Science, 241: 456 (1988); Dervan et al., Science, 251:1360 (1991)), thereby preventing transcription and the production of the PRO polypeptide. The antisense RNA oligonucleotide hybridizes to the mRNA *in vivo* and blocks translation of the mRNA molecule into the PRO polypeptide (antisense - Okano, Neurochem., 56:560 (1991); Oligodeoxynucleotides as Antisense Inhibitors of Gene Expression (CRC Press: Boca Raton, FL, 1988). The oligonucleotides described above can also be delivered to cells such that the antisense RNA or DNA may be expressed *in vivo* to inhibit production of the PRO polypeptide. When antisense DNA is used, oligodeoxyribonucleotides derived from the translation-initiation site, e.g., between about -10 and +10 positions of the target gene nucleotide sequence, are preferred.

Potential antagonists include small molecules that bind to the active site, the receptor binding site, or growth factor or other relevant binding site of the PRO polypeptide, thereby blocking the normal biological activity of the PRO polypeptide. Examples of small molecules include, but are not limited to, small peptides or peptide-like molecules, preferably soluble peptides, and synthetic non-peptidyl organic or inorganic compounds.

Ribozymes are enzymatic RNA molecules capable of catalyzing the specific cleavage of RNA. Ribozymes act by sequence-specific hybridization to the complementary target RNA, followed by endonucleolytic cleavage. Specific ribozyme cleavage sites within a potential RNA target can be identified by known techniques. For further details see, e.g., Rossi, Current Biology, 4:469-471 (1994), and PCT publication No. WO 97/33551 (published September 18, 1997).

Nucleic acid molecules in triple-helix formation used to inhibit transcription should be single-stranded and composed of deoxynucleotides. The base composition of these oligonucleotides is designed such that it promotes triple-helix formation via Hoogsteen base-pairing rules, which generally require sizeable stretches of purines or pyrimidines on one strand of a duplex. For further details see, e.g., PCT publication No. WO 97/33551, *supra*.

These small molecules can be identified by any one or more of the screening assays discussed hereinabove and/or by any other screening techniques well known for those skilled in the art.

Diagnostic and therapeutic uses of the herein disclosed molecules may also be based upon the positive functional assay hits disclosed and described below.

## F. Anti-PRO Antibodies

The present invention further provides anti-PRO antibodies. Exemplary antibodies include polyclonal, monoclonal, humanized, bispecific, and heteroconjugate antibodies.

### 1. Polyclonal Antibodies

The anti-PRO antibodies may comprise polyclonal antibodies. Methods of preparing polyclonal antibodies are known to the skilled artisan. Polyclonal antibodies can be raised in a mammal, for example, by one or more injections of an immunizing agent and, if desired, an adjuvant. Typically, the immunizing agent and/or adjuvant will be injected in the mammal by multiple subcutaneous or intraperitoneal injections. The immunizing agent may include the PRO polypeptide or a fusion protein thereof. It may be useful to conjugate the immunizing agent to a protein known to be immunogenic in the mammal being immunized. Examples of such immunogenic proteins include but are not limited to keyhole limpet hemocyanin, serum albumin, bovine thyroglobulin, and soybean trypsin inhibitor. Examples of adjuvants which may be employed include Freund's complete adjuvant and MPL-TDM adjuvant (monophosphoryl Lipid A, synthetic trehalose dicorynomycolate). The immunization protocol may be selected by one skilled in the art without undue experimentation.

### 2. Monoclonal Antibodies

The anti-PRO antibodies may, alternatively, be monoclonal antibodies. Monoclonal antibodies may be prepared using hybridoma methods, such as those described by Kohler and Milstein, Nature, 256:495 (1975). In a hybridoma method, a mouse, hamster, or other appropriate host animal, is typically immunized with an immunizing agent to elicit lymphocytes that produce or are capable of producing antibodies that will specifically bind to the immunizing agent. Alternatively, the lymphocytes may be immunized *in vitro*.

The immunizing agent will typically include the PRO polypeptide or a fusion protein thereof. Generally,

either peripheral blood lymphocytes ("PBLs") are used if cells of human origin are desired, or spleen cells or lymph node cells are used if non-human mammalian sources are desired. The lymphocytes are then fused with an immortalized cell line using a suitable fusing agent, such as polyethylene glycol, to form a hybridoma cell [Goding, Monoclonal Antibodies: Principles and Practice, Academic Press, (1986) pp. 59-103]. Immortalized cell lines are usually transformed mammalian cells, particularly myeloma cells of rodent, bovine and human origin. Usually, rat or mouse myeloma cell lines are employed. The hybridoma cells may be cultured in a suitable culture medium that preferably contains one or more substances that inhibit the growth or survival of the unfused, immortalized cells. For example, if the parental cells lack the enzyme hypoxanthine guanine phosphoribosyl transferase (HGPRT or HPRT), the culture medium for the hybridomas typically will include hypoxanthine, aminopterin, and thymidine ("HAT medium"), which substances prevent the growth of HGPRT-deficient cells.

Preferred immortalized cell lines are those that fuse efficiently, support stable high level expression of antibody by the selected antibody-producing cells, and are sensitive to a medium such as HAT medium. More preferred immortalized cell lines are murine myeloma lines, which can be obtained, for instance, from the Salk Institute Cell Distribution Center, San Diego, California and the American Type Culture Collection, Manassas, Virginia. Human myeloma and mouse-human heteromyeloma cell lines also have been described for the production of human monoclonal antibodies [Kozbor, J. Immunol., 133:3001 (1984); Brodeur et al., Monoclonal Antibody Production Techniques and Applications, Marcel Dekker, Inc., New York, (1987) pp. 51-63].

The culture medium in which the hybridoma cells are cultured can then be assayed for the presence of monoclonal antibodies directed against PRO. Preferably, the binding specificity of monoclonal antibodies produced by the hybridoma cells is determined by immunoprecipitation or by an *in vitro* binding assay, such as radioimmunoassay (RIA) or enzyme-linked immunoabsorbent assay (ELISA). Such techniques and assays are known in the art. The binding affinity of the monoclonal antibody can, for example, be determined by the Scatchard analysis of Munson and Pollard, Anal. Biochem., 107:220 (1980).

After the desired hybridoma cells are identified, the clones may be subcloned by limiting dilution procedures and grown by standard methods [Goding, supra]. Suitable culture media for this purpose include, for example, Dulbecco's Modified Eagle's Medium and RPMI-1640 medium. Alternatively, the hybridoma cells may be grown *in vivo* as ascites in a mammal.

The monoclonal antibodies secreted by the subclones may be isolated or purified from the culture medium or ascites fluid by conventional immunoglobulin purification procedures such as, for example, protein A-Sepharose, hydroxylapatite chromatography, gel electrophoresis, dialysis, or affinity chromatography.

The monoclonal antibodies may also be made by recombinant DNA methods, such as those described in U.S. Patent No. 4,816,567. DNA encoding the monoclonal antibodies of the invention can be readily isolated and sequenced using conventional procedures (e.g., by using oligonucleotide probes that are capable of binding specifically to genes encoding the heavy and light chains of murine antibodies). The hybridoma cells of the invention serve as a preferred source of such DNA. Once isolated, the DNA may be placed into expression vectors, which are then transfected into host cells such as simian COS cells, Chinese hamster ovary (CHO) cells, or myeloma cells that do not otherwise produce immunoglobulin protein, to obtain the synthesis of monoclonal

antibodies in the recombinant host cells. The DNA also may be modified, for example, by substituting the coding sequence for human heavy and light chain constant domains in place of the homologous murine sequences [U.S. Patent No. 4,816,567; Morrison et al., supra] or by covalently joining to the immunoglobulin coding sequence all or part of the coding sequence for a non-immunoglobulin polypeptide. Such a non-immunoglobulin polypeptide can be substituted for the constant domains of an antibody of the invention, or can be substituted for the variable domains of one antigen-combining site of an antibody of the invention to create a chimeric bivalent antibody.

The antibodies may be monovalent antibodies. Methods for preparing monovalent antibodies are well known in the art. For example, one method involves recombinant expression of immunoglobulin light chain and modified heavy chain. The heavy chain is truncated generally at any point in the Fc region so as to prevent heavy chain crosslinking. Alternatively, the relevant cysteine residues are substituted with another amino acid residue or are deleted so as to prevent crosslinking.

*In vitro* methods are also suitable for preparing monovalent antibodies. Digestion of antibodies to produce fragments thereof, particularly, Fab fragments, can be accomplished using routine techniques known in the art.

3. Human and Humanized Antibodies

The anti-PRO antibodies of the invention may further comprise humanized antibodies or human antibodies. Humanized forms of non-human (e.g., murine) antibodies are chimeric immunoglobulins, immunoglobulin chains or fragments thereof (such as Fv, Fab, Fab', $F(ab')_2$ or other antigen-binding subsequences of antibodies) which contain minimal sequence derived from non-human immunoglobulin. Humanized antibodies include human immunoglobulins (recipient antibody) in which residues from a complementary determining region (CDR) of the recipient are replaced by residues from a CDR of a non-human species (donor antibody) such as mouse, rat or rabbit having the desired specificity, affinity and capacity. In some instances, Fv framework residues of the human immunoglobulin are replaced by corresponding non-human residues. Humanized antibodies may also comprise residues which are found neither in the recipient antibody nor in the imported CDR or framework sequences. In general, the humanized antibody will comprise substantially all of at least one, and typically two, variable domains, in which all or substantially all of the CDR regions correspond to those of a non-human immunoglobulin and all or substantially all of the FR regions are those of a human immunoglobulin consensus sequence. The humanized antibody optimally also will comprise at least a portion of an immunoglobulin constant region (Fc), typically that of a human immunoglobulin [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-329 (1988); and Presta, Curr. Op. Struct. Biol., 2:593-596 (1992)].

Methods for humanizing non-human antibodies are well known in the art. Generally, a humanized antibody has one or more amino acid residues introduced into it from a source which is non-human. These non-human amino acid residues are often referred to as "import" residues, which are typically taken from an "import" variable domain. Humanization can be essentially performed following the method of Winter and co-workers [Jones et al., Nature, 321:522-525 (1986); Riechmann et al., Nature, 332:323-327 (1988); Verhoeyen et al., Science, 239:1534-1536 (1988)], by substituting rodent CDRs or CDR sequences for the corresponding sequences

of a human antibody. Accordingly, such "humanized" antibodies are chimeric antibodies (U.S. Patent No. 4,816,567), wherein substantially less than an intact human variable domain has been substituted by the corresponding sequence from a non-human species. In practice, humanized antibodies are typically human antibodies in which some CDR residues and possibly some FR residues are substituted by residues from analogous sites in rodent antibodies.

Human antibodies can also be produced using various techniques known in the art, including phage display libraries [Hoogenboom and Winter, J. Mol. Biol., 227:381 (1991); Marks et al., J. Mol. Biol., 222:581 (1991)]. The techniques of Cole et al. and Boerner et al. are also available for the preparation of human monoclonal antibodies (Cole et al., Monoclonal Antibodies and Cancer Therapy, Alan R. Liss, p. 77 (1985) and Boerner et al., J. Immunol., 147(1):86-95 (1991)]. Similarly, human antibodies can be made by introducing of human immunoglobulin loci into transgenic animals, e.g., mice in which the endogenous immunoglobulin genes have been partially or completely inactivated. Upon challenge, human antibody production is observed, which closely resembles that seen in humans in all respects, including gene rearrangement, assembly, and antibody repertoire. This approach is described, for example, in U.S. Patent Nos. 5,545,807; 5,545,806; 5,569,825; 5,625,126; 5,633,425; 5,661,016, and in the following scientific publications: Marks *et al.*, Bio/Technology 10, 779-783 (1992); Lonberg *et al.*, Nature 368 856-859 (1994); Morrison, Nature 368, 812-13 (1994); Fishwild *et al.*, Nature Biotechnology 14, 845-51 (1996); Neuberger, Nature Biotechnology 14, 826 (1996); Lonberg and Huszar, Intern. Rev. Immunol. 13 65-93 (1995).

The antibodies may also be affinity matured using known selection and/or mutagenesis methods as described above. Preferred affinity matured antibodies have an affinity which is five times, more preferably 10 times, even more preferably 20 or 30 times greater than the starting antibody (generally murine, humanized or human) from which the matured antibody is prepared.

4. Bispecific Antibodies

Bispecific antibodies are monoclonal, preferably human or humanized, antibodies that have binding specificities for at least two different antigens. In the present case, one of the binding specificities is for the PRO, the other one is for any other antigen, and preferably for a cell-surface protein or receptor or receptor subunit.

Methods for making bispecific antibodies are known in the art. Traditionally, the recombinant production of bispecific antibodies is based on the co-expression of two immunoglobulin heavy-chain/light-chain pairs, where the two heavy chains have different specificities [Milstein and Cuello, Nature, 305:537-539 (1983)]. Because of the random assortment of immunoglobulin heavy and light chains, these hybridomas (quadromas) produce a potential mixture of ten different antibody molecules, of which only one has the correct bispecific structure. The purification of the correct molecule is usually accomplished by affinity chromatography steps. Similar procedures are disclosed in WO 93/08829, published 13 May 1993, and in Traunecker et al., EMBO J., 10:3655-3659 (1991).

Antibody variable domains with the desired binding specificities (antibody-antigen combining sites) can be fused to immunoglobulin constant domain sequences. The fusion preferably is with an immunoglobulin heavy-chain constant domain, comprising at least part of the hinge, CH2, and CH3 regions. It is preferred to have the

first heavy-chain constant region (CH1) containing the site necessary for light-chain binding present in at least one of the fusions. DNAs encoding the immunoglobulin heavy-chain fusions and, if desired, the immunoglobulin light chain, are inserted into separate expression vectors, and are co-transfected into a suitable host organism. For further details of generating bispecific antibodies see, for example, Suresh et al., Methods in Enzymology, 121:210 (1986).

According to another approach described in WO 96/27011, the interface between a pair of antibody molecules can be engineered to maximize the percentage of heterodimers which are recovered from recombinant cell culture. The preferred interface comprises at least a part of the CH3 region of an antibody constant domain. In this method, one or more small amino acid side chains from the interface of the first antibody molecule are replaced with larger side chains (e.g. tyrosine or tryptophan). Compensatory "cavities" of identical or similar size to the large side chain(s) are created on the interface of the second antibody molecule by replacing large amino acid side chains with smaller ones (e.g. alanine or threonine). This provides a mechanism for increasing the yield of the heterodimer over other unwanted end-products such as homodimers.

Bispecific antibodies can be prepared as full length antibodies or antibody fragments (e.g. $F(ab')_2$ bispecific antibodies). Techniques for generating bispecific antibodies from antibody fragments have been described in the literature. For example, bispecific antibodies can be prepared can be prepared using chemical linkage. Brennan *et al.*, Science 229:81 (1985) describe a procedure wherein intact antibodies are proteolytically cleaved to generate $F(ab')_2$ fragments. These fragments are reduced in the presence of the dithiol complexing agent sodium arsenite to stabilize vicinal dithiols and prevent intermolecular disulfide formation. The Fab' fragments generated are then converted to thionitrobenzoate (TNB) derivatives. One of the Fab'-TNB derivatives is then reconverted to the Fab'-thiol by reduction with mercaptoethylamine and is mixed with an equimolar amount of the other Fab'-TNB derivative to form the bispecific antibody. The bispecific antibodies produced can be used as agents for the selective immobilization of enzymes.

Fab' fragments may be directly recovered from *E. coli* and chemically coupled to form bispecific antibodies. Shalaby *et al.*, J. Exp. Med. 175:217-225 (1992) describe the production of a fully humanized bispecific antibody $F(ab')_2$ molecule. Each Fab' fragment was separately secreted from *E. coli* and subjected to directed chemical coupling *in vitro* to form the bispecific antibody. The bispecific antibody thus formed was able to bind to cells overexpressing the ErbB2 receptor and normal human T cells, as well as trigger the lytic activity of human cytotoxic lymphocytes against human breast tumor targets.

Various technique for making and isolating bispecific antibody fragments directly from recombinant cell culture have also been described. For example, bispecific antibodies have been produced using leucine zippers. Kostelny *et al.*, J. Immunol. 148(5):1547-1553 (1992). The leucine zipper peptides from the Fos and Jun proteins were linked to the Fab' portions of two different antibodies by gene fusion. The antibody homodimers were reduced at the hinge region to form monomers and then re-oxidized to form the antibody heterodimers. This method can also be utilized for the production of antibody homodimers. The "diabody" technology described by Hollinger *et al.*, Proc. Natl. Acad. Sci. USA 90:6444-6448 (1993) has provided an alternative mechanism for making bispecific antibody fragments. The fragments comprise a heavy-chain variable domain ($V_H$) connected to a light-chain variable domain ($V_L$) by a linker which is too short to allow pairing between the two domains on

the same chain. Accordingly, the $V_H$ and $V_L$ domains of one fragment are forced to pair with the complementary $V_L$ and $V_H$ domains of another fragment, thereby forming two antigen-binding sites. Another strategy for making bispecific antibody fragments by the use of single-chain Fv (sFv) dimers has also been reported. See, Gruber *et al.*, J. Immunol. 152:5368 (1994).

Antibodies with more than two valencies are contemplated. For example, trispecific antibodies can be prepared. Tutt *et al.*, J. Immunol. 147:60 (1991).

Exemplary bispecific antibodies may bind to two different epitopes on a given PRO polypeptide herein. Alternatively, an anti-PRO polypeptide arm may be combined with an arm which binds to a triggering molecule on a leukocyte such as a T-cell receptor molecule (e.g. CD2, CD3, CD28, or B7), or Fc receptors for IgG (FcγR), such as FcγRI (CD64), FcγRII (CD32) and FcγRIII (CD16) so as to focus cellular defense mechanisms to the cell expressing the particular PRO polypeptide. Bispecific antibodies may also be used to localize cytotoxic agents to cells which express a particular PRO polypeptide. These antibodies possess a PRO-binding arm and an arm which binds a cytotoxic agent or a radionuclide chelator, such as EOTUBE, DPTA, DOTA, or TETA. Another bispecific antibody of interest binds the PRO polypeptide and further binds tissue factor (TF).

5. Heteroconjugate Antibodies

Heteroconjugate antibodies are also within the scope of the present invention. Heteroconjugate antibodies are composed of two covalently joined antibodies. Such antibodies have, for example, been proposed to target immune system cells to unwanted cells [U.S. Patent No. 4,676,980], and for treatment of HIV infection [WO 91/00360; WO 92/200373; EP 03089]. It is contemplated that the antibodies may be prepared *in vitro* using known methods in synthetic protein chemistry, including those involving crosslinking agents. For example, immunotoxins may be constructed using a disulfide exchange reaction or by forming a thioether bond. Examples of suitable reagents for this purpose include iminothiolate and methyl-4-mercaptobutyrimidate and those disclosed, for example, in U.S. Patent No. 4,676,980.

6. Effector Function Engineering

It may be desirable to modify the antibody of the invention with respect to effector function, so as to enhance, *e.g.*, the effectiveness of the antibody in treating cancer. For example, cysteine residue(s) may be introduced into the Fc region, thereby allowing interchain disulfide bond formation in this region. The homodimeric antibody thus generated may have improved internalization capability and/or increased complement-mediated cell killing and antibody-dependent cellular cytotoxicity (ADCC). See Caron *et al.*, J. Exp Med., 176: 1191-1195 (1992) and Shopes, J. Immunol., 148: 2918-2922 (1992). Homodimeric antibodies with enhanced anti-tumor activity may also be prepared using heterobifunctional cross-linkers as described in Wolff *et al.* Cancer Research, 53: 2560-2565 (1993). Alternatively, an antibody can be engineered that has dual Fc regions and may thereby have enhanced complement lysis and ADCC capabilities. See Stevenson *et al.*, Anti-Cancer Drug Design, 3: 219-230 (1989).

7. Immunoconjugates

The invention also pertains to immunoconjugates comprising an antibody conjugated to a cytotoxic agent such as a chemotherapeutic agent, toxin (*e.g.*, an enzymatically active toxin of bacterial, fungal, plant, or animal origin, or fragments thereof), or a radioactive isotope (*i.e.*, a radioconjugate).

Chemotherapeutic agents useful in the generation of such immunoconjugates have been described above. Enzymatically active toxins and fragments thereof that can be used include diphtheria A chain, nonbinding active fragments of diphtheria toxin, exotoxin A chain (from *Pseudomonas aeruginosa*), ricin A chain, abrin A chain, modeccin A chain, alpha-sarcin, *Aleurites fordii* proteins, dianthin proteins, *Phytolaca americana* proteins (PAPI, PAPII, and PAP-S), momordica charantia inhibitor, curcin, crotin, sapaonaria officinalis inhibitor, gelonin, mitogellin, restrictocin, phenomycin, enomycin, and the tricothecenes. A variety of radionuclides are available for the production of radioconjugated antibodies. Examples include $^{212}Bi$, $^{131}I$, $^{131}In$, $^{90}Y$, and $^{186}Re$. Conjugates of the antibody and cytotoxic agent are made using a variety of bifunctional protein-coupling agents such as N-succinimidyl-3-(2-pyridyldithiol) propionate (SPDP), iminothiolane (IT), bifunctional derivatives of imidoesters (such as dimethyl adipimidate HCL), active esters (such as disuccinimidyl suberate), aldehydes (such as glutareldehyde), bis-azido compounds (such as bis (p-azidobenzoyl) hexanediamine), bis-diazonium derivatives (such as bis-(p-diazoniumbenzoyl)-ethylenediamine), diisocyanates (such as tolyene 2,6-diisocyanate), and bis-active fluorine compounds (such as 1,5-difluoro-2,4-dinitrobenzene). For example, a ricin immunotoxin can be prepared as described in Vitetta *et al.*, Science, 238: 1098 (1987). Carbon-14-labeled 1-isothiocyanatobenzyl-3-methyldiethylene triaminepentaacetic acid (MX-DTPA) is an exemplary chelating agent for conjugation of radionucleotide to the antibody. See WO94/11026.

In another embodiment, the antibody may be conjugated to a "receptor" (such streptavidin) for utilization in tumor pretargeting wherein the antibody-receptor conjugate is administered to the patient, followed by removal of unbound conjugate from the circulation using a clearing agent and then administration of a "ligand" (*e.g.*, avidin) that is conjugated to a cytotoxic agent (*e.g.*, a radionucleotide).

8. Immunoliposomes

The antibodies disclosed herein may also be formulated as immunoliposomes. Liposomes containing the antibody are prepared by methods known in the art, such as described in Epstein *et al.*, Proc. Natl. Acad. Sci. USA, 82: 3688 (1985); Hwang *et al.*, Proc. Natl Acad. Sci. USA, 77: 4030 (1980); and U.S. Pat. Nos. 4,485,045 and 4,544,545. Liposomes with enhanced circulation time are disclosed in U.S. Patent No. 5,013,556.

Particularly useful liposomes can be generated by the reverse-phase evaporation method with a lipid composition comprising phosphatidylcholine, cholesterol, and PEG-derivatized phosphatidylethanolamine (PEG-PE). Liposomes are extruded through filters of defined pore size to yield liposomes with the desired diameter. Fab' fragments of the antibody of the present invention can be conjugated to the liposomes as described in Martin *et al.*, J. Biol. Chem., 257: 286-288 (1982) via a disulfide-interchange reaction. A chemotherapeutic agent (such as Doxorubicin) is optionally contained within the liposome. See Gabizon *et al.*, J. National Cancer Inst., 81(19): 1484 (1989).

9. Pharmaceutical Compositions of Antibodies

Antibodies specifically binding a PRO polypeptide identified herein, as well as other molecules identified by the screening assays disclosed hereinbefore, can be administered for the treatment of various disorders in the form of pharmaceutical compositions.

If the PRO polypeptide is intracellular and whole antibodies are used as inhibitors, internalizing antibodies are preferred. However, lipofections or liposomes can also be used to deliver the antibody, or an antibody fragment, into cells. Where antibody fragments are used, the smallest inhibitory fragment that specifically binds to the binding domain of the target protein is preferred. For example, based upon the variable-region sequences of an antibody, peptide molecules can be designed that retain the ability to bind the target protein sequence. Such peptides can be synthesized chemically and/or produced by recombinant DNA technology. See, *e.g.*, Marasco *et al.*, Proc. Natl. Acad. Sci. USA, 90: 7889-7893 (1993). The formulation herein may also contain more than one active compound as necessary for the particular indication being treated, preferably those with complementary activities that do not adversely affect each other. Alternatively, or in addition, the composition may comprise an agent that enhances its function, such as, for example, a cytotoxic agent, cytokine, chemotherapeutic agent, or growth-inhibitory agent. Such molecules are suitably present in combination in amounts that are effective for the purpose intended.

The active ingredients may also be entrapped in microcapsules prepared, for example, by coacervation techniques or by interfacial polymerization, for example, hydroxymethylcellulose or gelatin-microcapsules and poly-(methylmethacylate) microcapsules, respectively, in colloidal drug delivery systems (for example, liposomes, albumin microspheres, microemulsions, nano-particles, and nanocapsules) or in macroemulsions. Such techniques are disclosed in Remington's Pharmaceutical Sciences, *supra*.

The formulations to be used for *in vivo* administration must be sterile. This is readily accomplished by filtration through sterile filtration membranes.

Sustained-release preparations may be prepared. Suitable examples of sustained-release preparations include semipermeable matrices of solid hydrophobic polymers containing the antibody, which matrices are in the form of shaped articles, *e.g.*, films, or microcapsules. Examples of sustained-release matrices include polyesters, hydrogels (for example, poly(2-hydroxyethyl-methacrylate), or poly(vinylalcohol)), polylactides (U.S. Pat. No. 3,773,919), copolymers of L-glutamic acid and γ ethyl-L-glutamate, non-degradable ethylene-vinyl acetate, degradable lactic acid-glycolic acid copolymers such as the LUPRON DEPOT ™ (injectable microspheres composed of lactic acid-glycolic acid copolymer and leuprolide acetate), and poly-D-(-)-3-hydroxybutyric acid. While polymers such as ethylene-vinyl acetate and lactic acid-glycolic acid enable release of molecules for over 100 days, certain hydrogels release proteins for shorter time periods. When encapsulated antibodies remain in the body for a long time, they may denature or aggregate as a result of exposure to moisture at 37°C, resulting in a loss of biological activity and possible changes in immunogenicity. Rational strategies can be devised for stabilization depending on the mechanism involved. For example, if the aggregation mechanism is discovered to be intermolecular S-S bond formation through thio-disulfide interchange, stabilization may be achieved by modifying sulfhydryl residues, lyophilizing from acidic solutions, controlling moisture content, using appropriate additives, and developing specific polymer matrix compositions.

G. Uses for anti-PRO Antibodies

The anti-PRO antibodies of the invention have various utilities. For example, anti-PRO antibodies may be used in diagnostic assays for PRO, *e.g.*, detecting its expression (and in some cases, differential expression) in specific cells, tissues, or serum. Various diagnostic assay techniques known in the art may be used, such as competitive binding assays, direct or indirect sandwich assays and immunoprecipitation assays conducted in either heterogeneous or homogeneous phases [Zola, Monoclonal Antibodies: A Manual of Techniques, CRC Press, Inc. (1987) pp. 147-158]. The antibodies used in the diagnostic assays can be labeled with a detectable moiety. The detectable moiety should be capable of producing, either directly or indirectly, a detectable signal. For example, the detectable moiety may be a radioisotope, such as $^{3}H$, $^{14}C$, $^{32}P$, $^{35}S$, or $^{125}I$, a fluorescent or chemiluminescent compound, such as fluorescein isothiocyanate, rhodamine, or luciferin, or an enzyme, such as alkaline phosphatase, beta-galactosidase or horseradish peroxidase. Any method known in the art for conjugating the antibody to the detectable moiety may be employed, including those methods described by Hunter et al., Nature, 144:945 (1962); David et al., Biochemistry, 13:1014 (1974); Pain et al., J. Immunol. Meth., 40:219 (1981); and Nygren, J. Histochem. and Cytochem., 30:407 (1982).

Anti-PRO antibodies also are useful for the affinity purification of PRO from recombinant cell culture or natural sources. In this process, the antibodies against PRO are immobilized on a suitable support, such a Sephadex resin or filter paper, using methods well known in the art. The immobilized antibody then is contacted with a sample containing the PRO to be purified, and thereafter the support is washed with a suitable solvent that will remove substantially all the material in the sample except the PRO, which is bound to the immobilized antibody. Finally, the support is washed with another suitable solvent that will release the PRO from the antibody.

The following examples are offered for illustrative purposes only, and are not intended to limit the scope of the present invention in any way.

All patent and literature references cited in the present specification are hereby incorporated by reference in their entirety.

## EXAMPLES

Commercially available reagents referred to in the examples were used according to manufacturer's instructions unless otherwise indicated. The source of those cells identified in the following examples, and throughout the specification, by ATCC accession numbers is the American Type Culture Collection, Manassas, VA.

### EXAMPLE 1: Extracellular Domain Homology Screening to Identify Novel Polypeptides and cDNA Encoding Therefor

The extracellular domain (ECD) sequences (including the secretion signal sequence, if any) from about 950 known secreted proteins from the Swiss-Prot public database were used to search EST databases. The EST databases included public databases (*e.g.*, Dayhoff, GenBank), and proprietary databases (e.g. LIFESEQ™, Incyte Pharmaceuticals, Palo Alto, CA). The search was performed using the computer program BLAST or

BLAST-2 (Altschul *et al.*, Methods in Enzymology, 266:460-480 (1996)) as a comparison of the ECD protein sequences to a 6 frame translation of the EST sequences. Those comparisons with a BLAST score of 70 (or in some cases 90) or greater that did not encode known proteins were clustered and assembled into consensus DNA sequences with the program "phrap" (Phil Green, University of Washington, Seattle, WA).

Using this extracellular domain homology screen, consensus DNA sequences were assembled relative to the other identified EST sequences using phrap. In addition, the consensus DNA sequences obtained were often (but not always) extended using repeated cycles of BLAST or BLAST-2 and phrap to extend the consensus sequence as far as possible using the sources of EST sequences discussed above.

Based upon the consensus sequences obtained as described above, oligonucleotides were then synthesized and used to identify by PCR a cDNA library that contained the sequence of interest and for use as probes to isolate a clone of the full-length coding sequence for a PRO polypeptide. Forward and reverse PCR primers generally range from 20 to 30 nucleotides and are often designed to give a PCR product of about 100-1000 bp in length. The probe sequences are typically 40-55 bp in length. In some cases, additional oligonucleotides are synthesized when the consensus sequence is greater than about 1-1.5kbp. In order to screen several libraries for a full-length clone, DNA from the libraries was screened by PCR amplification, as per Ausubel *et al.*, Current Protocols in Molecular Biology, with the PCR primer pair. A positive library was then used to isolate clones encoding the gene of interest using the probe oligonucleotide and one of the primer pairs.

The cDNA libraries used to isolate the cDNA clones were constructed by standard methods using commercially available reagents such as those from Invitrogen, San Diego, CA. The cDNA was primed with oligo dT containing a NotI site, linked with blunt to SalI hemikinased adaptors, cleaved with NotI, sized appropriately by gel electrophoresis, and cloned in a defined orientation into a suitable cloning vector (such as pRKB or pRKD; pRK5B is a precursor of pRK5D that does not contain the SfiI site; *see*, Holmes *et al.*, Science, 253:1278-1280 (1991)) in the unique XhoI and NotI sites.

EXAMPLE 2: Isolation of cDNA clones by Amylase Screening

1. Preparation of oligo dT primed cDNA library

mRNA was isolated from a human tissue of interest using reagents and protocols from Invitrogen, San Diego, CA (Fast Track 2). This RNA was used to generate an oligo dT primed cDNA library in the vector pRK5D using reagents and protocols from Life Technologies, Gaithersburg, MD (Super Script Plasmid System). In this procedure, the double stranded cDNA was sized to greater than 1000 bp and the SalI/NotI linkered cDNA was cloned into XhoI/NotI cleaved vector. pRK5D is a cloning vector that has an sp6 transcription initiation site followed by an SfiI restriction enzyme site preceding the XhoI/NotI cDNA cloning sites.

2. Preparation of random primed cDNA library

A secondary cDNA library was generated in order to preferentially represent the 5' ends of the primary cDNA clones. Sp6 RNA was generated from the primary library (described above), and this RNA was used to generate a random primed cDNA library in the vector pSST-AMY.0 using reagents and protocols from Life Technologies (Super Script Plasmid System, referenced above). In this procedure the double stranded cDNA was

sized to 500-1000 bp, linkered with blunt to NotI adaptors, cleaved with SfiI, and cloned into SfiI/NotI cleaved vector. pSST-AMY.0 is a cloning vector that has a yeast alcohol dehydrogenase promoter preceding the cDNA cloning sites and the mouse amylase sequence (the mature sequence without the secretion signal) followed by the yeast alcohol dehydrogenase terminator, after the cloning sites. Thus, cDNAs cloned into this vector that are fused in frame with amylase sequence will lead to the secretion of amylase from appropriately transfected yeast colonies.

3. Transformation and Detection

DNA from the library described in paragraph 2 above was chilled on ice to which was added electrocompetent DH10B bacteria (Life Technologies, 20 ml). The bacteria and vector mixture was then electroporated as recommended by the manufacturer. Subsequently, SOC media (Life Technologies, 1 ml) was added and the mixture was incubated at 37°C for 30 minutes. The transformants were then plated onto 20 standard 150 mm LB plates containing ampicillin and incubated for 16 hours (37°C). Positive colonies were scraped off the plates and the DNA was isolated from the bacterial pellet using standard protocols, *e.g.* CsCl-gradient. The purified DNA was then carried on to the yeast protocols below.

The yeast methods were divided into three categories: (1) Transformation of yeast with the plasmid/cDNA combined vector; (2) Detection and isolation of yeast clones secreting amylase; and (3) PCR amplification of the insert directly from the yeast colony and purification of the DNA for sequencing and further analysis.

The yeast strain used was HD56-5A (ATCC-90785). This strain has the following genotype: MAT alpha, ura3-52, leu2-3, leu2-112, his3-11, his3-15, $MAL^+$, $SUC^+$, $GAL^+$. Preferably, yeast mutants can be employed that have deficient post-translational pathways. Such mutants may have translocation deficient alleles in *sec*71, *sec*72, *sec*62, with truncated *sec*71 being most preferred. Alternatively, antagonists (including antisense nucleotides and/or ligands) which interfere with the normal operation of these genes, other proteins implicated in this post translation pathway (e.g., SEC61p, SEC72p, SEC62p, SEC63p, TDJ1p or SSA1p-4p) or the complex formation of these proteins may also be preferably employed in combination with the amylase-expressing yeast.

Transformation was performed based on the protocol outlined by Gietz *et al.*, Nucl. Acid. Res., 20:1425 (1992). Transformed cells were then inoculated from agar into YEPD complex media broth (100 ml) and grown overnight at 30°C. The YEPD broth was prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 207 (1994). The overnight culture was then diluted to about $2 \times 10^6$ cells/ml (approx. $OD_{600}$=0.1) into fresh YEPD broth (500 ml) and regrown to $1 \times 10^7$ cells/ml (approx. $OD_{600}$=0.4-0.5).

The cells were then harvested and prepared for transformation by transfer into GS3 rotor bottles in a Sorval GS3 rotor at 5,000 rpm for 5 minutes, the supernatant discarded, and then resuspended into sterile water, and centrifuged again in 50 ml falcon tubes at 3,500 rpm in a Beckman GS-6KR centrifuge. The supernatant was discarded and the cells were subsequently washed with LiAc/TE (10 ml, 10 mM Tris-HCl, 1 mM EDTA pH 7.5, 100 mM $Li_2OOCCH_3$), and resuspended into LiAc/TE (2.5 ml).

Transformation took place by mixing the prepared cells (100 $\mu$l) with freshly denatured single stranded

salmon testes DNA (Lofstrand Labs, Gaithersburg, MD) and transforming DNA (1 μg, vol. < 10 μl) in microfuge tubes. The mixture was mixed briefly by vortexing, then 40% PEG/TE (600 μl, 40% polyethylene glycol-4000, 10 mM Tris-HCl, 1 mM EDTA, 100 mM $Li_2OOCCH_3$, pH 7.5) was added. This mixture was gently mixed and incubated at 30°C while agitating for 30 minutes. The cells were then heat shocked at 42°C for 15 minutes, and the reaction vessel centrifuged in a microfuge at 12,000 rpm for 5-10 seconds, decanted and resuspended into TE (500 μl, 10 mM Tris-HCl, 1 mM EDTA pH 7.5) followed by recentrifugation. The cells were then diluted into TE (1 ml) and aliquots (200 μl) were spread onto the selective media previously prepared in 150 mm growth plates (VWR).

Alternatively, instead of multiple small reactions, the transformation was performed using a single, large scale reaction, wherein reagent amounts were scaled up accordingly.

The selective media used was a synthetic complete dextrose agar lacking uracil (SCD-Ura) prepared as described in Kaiser *et al.*, Methods in Yeast Genetics, Cold Spring Harbor Press, Cold Spring Harbor, NY, p. 208-210 (1994). Transformants were grown at 30°C for 2-3 days.

The detection of colonies secreting amylase was performed by including red starch in the selective growth media. Starch was coupled to the red dye (Reactive Red-120, Sigma) as per the procedure described by Biely *et al.*, Anal. Biochem., 172:176-179 (1988). The coupled starch was incorporated into the SCD-Ura agar plates at a final concentration of 0.15% (w/v), and was buffered with potassium phosphate to a pH of 7.0 (50-100 mM final concentration).

The positive colonies were picked and streaked across fresh selective media (onto 150 mm plates) in order to obtain well isolated and identifiable single colonies. Well isolated single colonies positive for amylase secretion were detected by direct incorporation of red starch into buffered SCD-Ura agar. Positive colonies were determined by their ability to break down starch resulting in a clear halo around the positive colony visualized directly.

4. Isolation of DNA by PCR Amplification

When a positive colony was isolated, a portion of it was picked by a toothpick and diluted into sterile water (30 μl) in a 96 well plate. At this time, the positive colonies were either frozen and stored for subsequent analysis or immediately amplified. An aliquot of cells (5 μl) was used as a template for the PCR reaction in a 25 μl volume containing: 0.5 μl Klentaq (Clontech, Palo Alto, CA); 4.0 μl 10 mM dNTP's (Perkin Elmer-Cetus); 2.5 μl Kentaq buffer (Clontech); 0.25 μl forward oligo 1; 0.25 μl reverse oligo 2; 12.5 μl distilled water. The sequence of the forward oligonucleotide 1 was:

5'-TGTAAAACGACGGCCAGTTAAATAGACCTGCAATTATTAATCT-3' (SEQ ID NO:115)

The sequence of reverse oligonucleotide 2 was:

5'-CAGGAAACAGCTATGACCACCTGCACACCTGCAAATCCATT-3' (SEQ ID NO:116)

PCR was then performed as follows:

| | | | | |
|---|---|---|---|---|
| a. | | Denature | 92°C, | 5 minutes |
| b. | 3 cycles of: | Denature | 92°C, | 30 seconds |
| | | Anneal | 59°C, | 30 seconds |

| | | | | |
|---|---|---|---|---|
| | | | Extend | 72°C, 60 seconds |
| | c. | 3 cycles of: | Denature | 92°C, 30 seconds |
| | | | Anneal | 57°C, 30 seconds |
| | | | Extend | 72°C, 60 seconds |
| | d. | 25 cycles of: | Denature | 92°C, 30 seconds |
| | | | Anneal | 55°C, 30 seconds |
| | | | Extend | 72°C, 60 seconds |
| | e. | | Hold | 4°C |

The underlined regions of the oligonucleotides annealed to the ADH promoter region and the amylase region, respectively, and amplified a 307 bp region from vector pSST-AMY.0 when no insert was present. Typically, the first 18 nucleotides of the 5' end of these oligonucleotides contained annealing sites for the sequencing primers. Thus, the total product of the PCR reaction from an empty vector was 343 bp. However, signal sequence-fused cDNA resulted in considerably longer nucleotide sequences.

Following the PCR, an aliquot of the reaction (5 μl) was examined by agarose gel electrophoresis in a 1% agarose gel using a Tris-Borate-EDTA (TBE) buffering system as described by Sambrook *et al.*, *supra*. Clones resulting in a single strong PCR product larger than 400 bp were further analyzed by DNA sequencing after purification with a 96 Qiaquick PCR clean-up column (Qiagen Inc., Chatsworth, CA).

EXAMPLE 3: Isolation of cDNA Clones Using Signal Algorithm Analysis

Various polypeptide-encoding nucleic acid sequences were identified by applying a proprietary signal sequence finding algorithm developed by Genentech, Inc. (South San Francisco, CA) upon ESTs as well as clustered and assembled EST fragments from public (*e.g.*, GenBank) and/or private (LIFESEQ®, Incyte Pharmaceuticals, Inc., Palo Alto, CA) databases. The signal sequence algorithm computes a secretion signal score based on the character of the DNA nucleotides surrounding the first and optionally the second methionine codon(s) (ATG) at the 5'-end of the sequence or sequence fragment under consideration. The nucleotides following the first ATG must code for at least 35 unambiguous amino acids without any stop codons. If the first ATG has the required amino acids, the second is not examined. If neither meets the requirement, the candidate sequence is not scored. In order to determine whether the EST sequence contains an authentic signal sequence, the DNA and corresponding amino acid sequences surrounding the ATG codon are scored using a set of seven sensors (evaluation parameters) known to be associated with secretion signals. Use of this algorithm resulted in the identification of numerous polypeptide-encoding nucleic acid sequences.

EXAMPLE 4: Isolation of cDNA clones Encoding Human PRO Polypeptides

Using the techniques described in Examples 1 to 3 above, numerous full-length cDNA clones were identified as encoding PRO polypeptides as disclosed herein. These cDNAs were then deposited under the terms of the Budapest Treaty with the American Type Culture Collection, 10801 University Blvd., Manassas, VA 20110-2209, USA (ATCC) as shown in Table 7 below.

Table 7

| Material | ATCC Dep. No. | Deposit Date |
|---|---|---|
| DNA16422-1209 | 209929 | June 2, 1998 |
| DNA19902-1669 | 203454 | November 3, 1998 |
| DNA21624-1391 | 209917 | June 2, 1998 |
| DNA34387-1138 | 209260 | September 16, 1997 |
| DNA35880-1160 | 209379 | October 16, 1997 |
| DNA39984-1221 | 209435 | November 7, 1997 |
| DNA44189-1322 | 209699 | March 26, 1998 |
| DNA48303-2829 | PTA-1342 | February 8, 2000 |
| DNA48320-1433 | 209904 | May 27, 1998 |
| DNA56049-2543 | 203662 | February 9, 1999 |
| DNA57694-1341 | 203017 | June 23, 1998 |
| DNA59208-1373 | 209881 | May 20, 1998 |
| DNA59214-1449 | 203046 | July 1, 1998 |
| DNA59485-1336 | 203015 | June 23, 1998 |
| DNA64966-1575 | 203575 | January 12, 1999 |
| DNA 82403-2959 | PTA-2317 | August 1, 2000 |
| DNA83505-2606 | PTA-132 | May 25, 1999 |
| DNA84927-2585 | 203865 | March 23, 1999 |
| DNA92264-2616 | 203969 | April 27, 1999 |
| DNA94713-2561 | 203835 | March 9, 1999 |
| DNA96869-2673 | PTA-255 | June 22, 1999 |
| DNA96881-2699 | PTA-553 | August 17, 1999 |
| DNA96889-2641 | PTA-119 | May 25, 1999 |
| DNA96898-2640 | PTA-122 | May 25, 1999 |
| DNA97003-2649 | PTA-43 | May 11, 1999 |
| DNA98565-2701 | PTA-481 | August 3, 1999 |
| DNA102846-2742 | PTA-545 | August 17, 1999 |
| DNA102847-2726 | PTA-517 | August 10, 1999 |
| DNA102880-2689 | PTA-383 | July 20, 1999 |
| DNA105782-2683 | PTA-387 | July 20, 1999 |
| DNA108912-2680 | PTA-124 | May, 25, 1999 |
| DNA115253-2757 | PTA-612 | August 31, 1999 |
| DNA119302-2737 | PTA-520 | August 10, 1999 |
| DNA119536-2752 | PTA-551 | August 17, 1999 |
| DNA119542-2754 | PTA-619 | August 31, 1999 |

Table 7 (cont')

| Material | ATCC Dep. No. | Deposit Date |
|---|---|---|
| DNA143498-2824 | PTA-1263 | February 2, 2000 |
| DNA145583-2820 | PTA-1179 | January 11, 2000 |
| DNA161000-2896 | PTA-1731 | April 18, 2000 |
| DNA161005-2943 | PTA-2243 | June 27, 2000 |
| DNA170245-3053 | PTA-2952 | January 23, 2001 |
| DNA171771-2919 | PTA-1902 | May 23, 2000 |
| DNA173157-2981 | PTA-2388 | August 8, 2000 |
| DNA175734-2985 | PTA-2455 | September 12, 2000 |
| DNA176108-3040 | PTA-2824 | December 19, 2000 |
| DNA190710-3028 | PTA-2822 | December 19, 2000 |
| DNA190803-3019 | PTA-2785 | December 12, 2000 |
| DNA191064-3069 | PTA-3016 | February 6, 2001 |
| DNA194909-3013 | PTA-2779 | December 12, 2000 |
| DNA203532-3029 | PTA-2823 | December 19, 2000 |
| DNA213858-3060 | PTA-2958 | January 23, 2001 |
| DNA216676-3083 | PTA-3157 | March 6, 2001 |
| DNA222653-3104 | PTA-3330 | April 24, 2001 |
| DNA96897-2688 | PTA-379 | July 20, 1999 |
| DNA142917-3081 | PTA-3155 | March 6, 2001 |
| DNA142930-2914 | PTA-1901 | May 23, 2000 |
| DNA147253-2983 | PTA-2405 | August 22, 2000 |
| DNA149927-2887 | PTA-1782 | April 25, 2000 |

These deposits were made under the provisions of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purpose of Patent Procedure and the Regulations thereunder (Budapest Treaty). This assures maintenance of a viable culture of the deposit for 30 years from the date of deposit. The deposits will be made available by ATCC under the terms of the Budapest Treaty, and subject to an agreement between Genentech, Inc. and ATCC, which assures permanent and unrestricted availability of the progeny of the culture of the deposit to the public upon issuance of the pertinent U.S. patent or upon laying open to the public of any U.S. or foreign patent application, whichever comes first, and assures availability of the progeny to one determined by the U.S. Commissioner of Patents and Trademarks to be entitled thereto according to 35 USC § 122 and the Commissioner's rules pursuant thereto (including 37 CFR § 1.14 with particular reference to 886 OG 638).

The assignee of the present application has agreed that if a culture of the materials on deposit should die or be lost or destroyed when cultivated under suitable conditions, the materials will be promptly replaced on notification with another of the same. Availability of the deposited material is not to be construed as a license to practice the invention in contravention of the rights granted under the authority of any government in

accordance with its patent laws.

EXAMPLE 5: Use of PRO as a hybridization probe

The following method describes use of a nucleotide sequence encoding PRO as a hybridization probe.

DNA comprising the coding sequence of full-length or mature PRO as disclosed herein is employed as a probe to screen for homologous DNAs (such as those encoding naturally-occurring variants of PRO) in human tissue cDNA libraries or human tissue genomic libraries.

Hybridization and washing of filters containing either library DNAs is performed under the following high stringency conditions. Hybridization of radiolabeled PRO-derived probe to the filters is performed in a solution of 50% formamide, 5x SSC, 0.1% SDS, 0.1% sodium pyrophosphate, 50 mM sodium phosphate, pH 6.8, 2x Denhardt's solution, and 10% dextran sulfate at 42°C for 20 hours. Washing of the filters is performed in an aqueous solution of 0.1x SSC and 0.1% SDS at 42°C.

DNAs having a desired sequence identity with the DNA encoding full-length native sequence PRO can then be identified using standard techniques known in the art.

EXAMPLE 6: Expression of PRO in *E. coli*

This example illustrates preparation of an unglycosylated form of PRO by recombinant expression in *E. coli*.

The DNA sequence encoding PRO is initially amplified using selected PCR primers. The primers should contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector. A variety of expression vectors may be employed. An example of a suitable vector is pBR322 (derived from *E. coli*; see Bolivar et al., Gene, 2:95 (1977)) which contains genes for ampicillin and tetracycline resistance. The vector is digested with restriction enzyme and dephosphorylated. The PCR amplified sequences are then ligated into the vector. The vector will preferably include sequences which encode for an antibiotic resistance gene, a trp promoter, a polyhis leader (including the first six STII codons, polyhis sequence, and enterokinase cleavage site), the PRO coding region, lambda transcriptional terminator, and an argU gene.

The ligation mixture is then used to transform a selected *E. coli* strain using the methods described in Sambrook et al., supra. Transformants are identified by their ability to grow on LB plates and antibiotic resistant colonies are then selected. Plasmid DNA can be isolated and confirmed by restriction analysis and DNA sequencing.

Selected clones can be grown overnight in liquid culture medium such as LB broth supplemented with antibiotics. The overnight culture may subsequently be used to inoculate a larger scale culture. The cells are then grown to a desired optical density, during which the expression promoter is turned on.

After culturing the cells for several more hours, the cells can be harvested by centrifugation. The cell pellet obtained by the centrifugation can be solubilized using various agents known in the art, and the solubilized PRO protein can then be purified using a metal chelating column under conditions that allow tight binding of the protein.

PRO may be expressed in *E. coli* in a poly-His tagged form, using the following procedure. The DNA

encoding PRO is initially amplified using selected PCR primers. The primers will contain restriction enzyme sites which correspond to the restriction enzyme sites on the selected expression vector, and other useful sequences providing for efficient and reliable translation initiation, rapid purification on a metal chelation column, and proteolytic removal with enterokinase. The PCR-amplified, poly-His tagged sequences are then ligated into an expression vector, which is used to transform an *E. coli* host based on strain 52 (W3110 fuhA(tonA) lon galE rpoHts(htpRts) clpP(lacIq). Transformants are first grown in LB containing 50 mg/ml carbenicillin at 30°C with shaking until an O.D.600 of 3-5 is reached. Cultures are then diluted 50-100 fold into CRAP media (prepared by mixing 3.57 g $(NH_4)_2SO_4$, 0.71 g sodium citrate•2H2O, 1.07 g KCl, 5.36 g Difco yeast extract, 5.36 g Sheffield hycase SF in 500 mL water, as well as 110 mM MPOS, pH 7.3, 0.55% (w/v) glucose and 7 mM $MgSO_4$) and grown for approximately 20-30 hours at 30°C with shaking. Samples are removed to verify expression by SDS-PAGE analysis, and the bulk culture is centrifuged to pellet the cells. Cell pellets are frozen until purification and refolding.

*E. coli* paste from 0.5 to 1 L fermentations (6-10 g pellets) is resuspended in 10 volumes (w/v) in 7 M guanidine, 20 mM Tris, pH 8 buffer. Solid sodium sulfite and sodium tetrathionate is added to make final concentrations of 0.1M and 0.02 M, respectively, and the solution is stirred overnight at 4°C. This step results in a denatured protein with all cysteine residues blocked by sulfitolization. The solution is centrifuged at 40,000 rpm in a Beckman Ultracentifuge for 30 min. The supernatant is diluted with 3-5 volumes of metal chelate column buffer (6 M guanidine, 20 mM Tris, pH 7.4) and filtered through 0.22 micron filters to clarify. The clarified extract is loaded onto a 5 ml Qiagen Ni-NTA metal chelate column equilibrated in the metal chelate column buffer. The column is washed with additional buffer containing 50 mM imidazole (Calbiochem, Utrol grade), pH 7.4. The protein is eluted with buffer containing 250 mM imidazole. Fractions containing the desired protein are pooled and stored at 4°C. Protein concentration is estimated by its absorbance at 280 nm using the calculated extinction coefficient based on its amino acid sequence.

The proteins are refolded by diluting the sample slowly into freshly prepared refolding buffer consisting of: 20 mM Tris, pH 8.6, 0.3 M NaCl, 2.5 M urea, 5 mM cysteine, 20 mM glycine and 1 mM EDTA. Refolding volumes are chosen so that the final protein concentration is between 50 to 100 micrograms/ml. The refolding solution is stirred gently at 4°C for 12-36 hours. The refolding reaction is quenched by the addition of TFA to a final concentration of 0.4% (pH of approximately 3). Before further purification of the protein, the solution is filtered through a 0.22 micron filter and acetonitrile is added to 2-10% final concentration. The refolded protein is chromatographed on a Poros R1/H reversed phase column using a mobile buffer of 0.1% TFA with elution with a gradient of acetonitrile from 10 to 80%. Aliquots of fractions with A280 absorbance are analyzed on SDS polyacrylamide gels and fractions containing homogeneous refolded protein are pooled. Generally, the properly refolded species of most proteins are eluted at the lowest concentrations of acetonitrile since those species are the most compact with their hydrophobic interiors shielded from interaction with the reversed phase resin. Aggregated species are usually eluted at higher acetonitrile concentrations. In addition to resolving misfolded forms of proteins from the desired form, the reversed phase step also removes endotoxin from the samples.

Fractions containing the desired folded PRO polypeptide are pooled and the acetonitrile removed using a gentle stream of nitrogen directed at the solution. Proteins are formulated into 20 mM Hepes, pH 6.8 with 0.14

M sodium chloride and 4% mannitol by dialysis or by gel filtration using G25 Superfine (Pharmacia) resins equilibrated in the formulation buffer and sterile filtered.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 7: Expression of PRO in mammalian cells

This example illustrates preparation of a potentially glycosylated form of PRO by recombinant expression in mammalian cells.

The vector, pRK5 (see EP 307,247, published March 15, 1989), is employed as the expression vector. Optionally, the PRO DNA is ligated into pRK5 with selected restriction enzymes to allow insertion of the PRO DNA using ligation methods such as described in Sambrook et al., supra. The resulting vector is called pRK5-PRO.

In one embodiment, the selected host cells may be 293 cells. Human 293 cells (ATCC CCL 1573) are grown to confluence in tissue culture plates in medium such as DMEM supplemented with fetal calf serum and optionally, nutrient components and/or antibiotics. About 10 μg pRK5-PRO DNA is mixed with about 1 μg DNA encoding the VA RNA gene [Thimmappaya et al., Cell, 31:543 (1982)] and dissolved in 500 μl of 1 mM Tris-HCl, 0.1 mM EDTA, 0.227 M $CaCl_2$. To this mixture is added, dropwise, 500 μl of 50 mM HEPES (pH 7.35), 280 mM NaCl, 1.5 mM $NaPO_4$, and a precipitate is allowed to form for 10 minutes at 25°C. The precipitate is suspended and added to the 293 cells and allowed to settle for about four hours at 37°C. The culture medium is aspirated off and 2 ml of 20% glycerol in PBS is added for 30 seconds. The 293 cells are then washed with serum free medium, fresh medium is added and the cells are incubated for about 5 days.

Approximately 24 hours after the transfections, the culture medium is removed and replaced with culture medium (alone) or culture medium containing 200 μCi/ml $^{35}$S-cysteine and 200 μCi/ml $^{35}$S-methionine. After a 12 hour incubation, the conditioned medium is collected, concentrated on a spin filter, and loaded onto a 15% SDS gel. The processed gel may be dried and exposed to film for a selected period of time to reveal the presence of PRO polypeptide. The cultures containing transfected cells may undergo further incubation (in serum free medium) and the medium is tested in selected bioassays.

In an alternative technique, PRO may be introduced into 293 cells transiently using the dextran sulfate method described by Somparyrac et al., Proc. Natl. Acad. Sci., 12:7575 (1981). 293 cells are grown to maximal density in a spinner flask and 700 μg pRK5-PRO DNA is added. The cells are first concentrated from the spinner flask by centrifugation and washed with PBS. The DNA-dextran precipitate is incubated on the cell pellet for four hours. The cells are treated with 20% glycerol for 90 seconds, washed with tissue culture medium, and re-introduced into the spinner flask containing tissue culture medium, 5 μg/ml bovine insulin and 0.1 μg/ml bovine transferrin. After about four days, the conditioned media is centrifuged and filtered to remove cells and debris. The sample containing expressed PRO can then be concentrated and purified by any selected method, such as dialysis and/or column chromatography.

In another embodiment, PRO can be expressed in CHO cells. The pRK5-PRO can be transfected into CHO cells using known reagents such as $CaPO_4$ or DEAE-dextran. As described above, the cell cultures can be incubated, and the medium replaced with culture medium (alone) or medium containing a radiolabel such as $^{35}$S-

methionine. After determining the presence of PRO polypeptide, the culture medium may be replaced with serum free medium. Preferably, the cultures are incubated for about 6 days, and then the conditioned medium is harvested. The medium containing the expressed PRO can then be concentrated and purified by any selected method.

Epitope-tagged PRO may also be expressed in host CHO cells. The PRO may be subcloned out of the pRK5 vector. The subclone insert can undergo PCR to fuse in frame with a selected epitope tag such as a poly-his tag into a Baculovirus expression vector. The poly-his tagged PRO insert can then be subcloned into a SV40 driven vector containing a selection marker such as DHFR for selection of stable clones. Finally, the CHO cells can be transfected (as described above) with the SV40 driven vector. Labeling may be performed, as described above, to verify expression. The culture medium containing the expressed poly-His tagged PRO can then be concentrated and purified by any selected method, such as by $Ni^{2+}$-chelate affinity chromatography.

PRO may also be expressed in CHO and/or COS cells by a transient expression procedure or in CHO cells by another stable expression procedure.

Stable expression in CHO cells is performed using the following procedure. The proteins are expressed as an IgG construct (immunoadhesin), in which the coding sequences for the soluble forms (e.g. extracellular domains) of the respective proteins are fused to an IgG1 constant region sequence containing the hinge, CH2 and CH2 domains and/or is a poly-His tagged form.

Following PCR amplification, the respective DNAs are subcloned in a CHO expression vector using standard techniques as described in Ausubel et al., Current Protocols of Molecular Biology, Unit 3.16, John Wiley and Sons (1997). CHO expression vectors are constructed to have compatible restriction sites 5' and 3' of the DNA of interest to allow the convenient shuttling of cDNA's. The vector used expression in CHO cells is as described in Lucas et al., Nucl. Acids Res. 24:9 (1774-1779 (1996), and uses the SV40 early promoter/enhancer to drive expression of the cDNA of interest and dihydrofolate reductase (DHFR). DHFR expression permits selection for stable maintenance of the plasmid following transfection.

Twelve micrograms of the desired plasmid DNA is introduced into approximately 10 million CHO cells using commercially available transfection reagents Superfect® (Qiagen), Dosper® or Fugene® (Boehringer Mannheim). The cells are grown as described in Lucas et al., supra. Approximately $3 \times 10^7$ cells are frozen in an ampule for further growth and production as described below.

The ampules containing the plasmid DNA are thawed by placement into water bath and mixed by vortexing. The contents are pipetted into a centrifuge tube containing 10 mLs of media and centrifuged at 1000 rpm for 5 minutes. The supernatant is aspirated and the cells are resuspended in 10 mL of selective media (0.2 $\mu$m filtered PS20 with 5% 0.2 $\mu$m diafiltered fetal bovine serum). The cells are then aliquoted into a 100 mL spinner containing 90 mL of selective media. After 1-2 days, the cells are transferred into a 250 mL spinner filled with 150 mL selective growth medium and incubated at 37°C. After another 2-3 days, 250 mL, 500 mL and 2000 mL spinners are seeded with $3 \times 10^5$ cells/mL. The cell media is exchanged with fresh media by centrifugation and resuspension in production medium. Although any suitable CHO media may be employed, a production medium described in U.S. Patent No. 5,122,469, issued June 16, 1992 may actually be used. A 3L production spinner is seeded at $1.2 \times 10^6$ cells/mL. On day 0, the cell number pH ie determined. On day 1, the spinner is

sampled and sparging with filtered air is commenced. On day 2, the spinner is sampled, the temperature shifted to 33°C, and 30 mL of 500 g/L glucose and 0.6 mL of 10% antifoam (e.g., 35% polydimethylsiloxane emulsion, Dow Corning 365 Medical Grade Emulsion) taken. Throughout the production, the pH is adjusted as necessary to keep it at around 7.2. After 10 days, or until the viability dropped below 70%, the cell culture is harvested by centrifugation and filtering through a 0.22 $\mu$m filter. The filtrate was either stored at 4°C or immediately loaded onto columns for purification.

For the poly-His tagged constructs, the proteins are purified using a Ni-NTA column (Qiagen). Before purification, imidazole is added to the conditioned media to a concentration of 5 mM. The conditioned media is pumped onto a 6 ml Ni-NTA column equilibrated in 20 mM Hepes, pH 7.4, buffer containing 0.3 M NaCl and 5 mM imidazole at a flow rate of 4-5 ml/min. at 4°C. After loading, the column is washed with additional equilibration buffer and the protein eluted with equilibration buffer containing 0.25 M imidazole. The highly purified protein is subsequently desalted into a storage buffer containing 10 mM Hepes, 0.14 M NaCl and 4% mannitol, pH 6.8, with a 25 ml G25 Superfine (Pharmacia) column and stored at -80°C.

Immunoadhesin (Fc-containing) constructs are purified from the conditioned media as follows. The conditioned medium is pumped onto a 5 ml Protein A column (Pharmacia) which had been equilibrated in 20 mM Na phosphate buffer, pH 6.8. After loading, the column is washed extensively with equilibration buffer before elution with 100 mM citric acid, pH 3.5. The eluted protein is immediately neutralized by collecting 1 ml fractions into tubes containing 275 $\mu$L of 1 M Tris buffer, pH 9. The highly purified protein is subsequently desalted into storage buffer as described above for the poly-His tagged proteins. The homogeneity is assessed by SDS polyacrylamide gels and by N-terminal amino acid sequencing by Edman degradation.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 8: Expression of PRO in Yeast

The following method describes recombinant expression of PRO in yeast.

First, yeast expression vectors are constructed for intracellular production or secretion of PRO from the ADH2/GAPDH promoter. DNA encoding PRO and the promoter is inserted into suitable restriction enzyme sites in the selected plasmid to direct intracellular expression of PRO. For secretion, DNA encoding PRO can be cloned into the selected plasmid, together with DNA encoding the ADH2/GAPDH promoter, a native PRO signal peptide or other mammalian signal peptide, or, for example, a yeast alpha-factor or invertase secretory signal/leader sequence, and linker sequences (if needed) for expression of PRO.

Yeast cells, such as yeast strain AB110, can then be transformed with the expression plasmids described above and cultured in selected fermentation media. The transformed yeast supernatants can be analyzed by precipitation with 10% trichloroacetic acid and separation by SDS-PAGE, followed by staining of the gels with Coomassie Blue stain.

Recombinant PRO can subsequently be isolated and purified by removing the yeast cells from the fermentation medium by centrifugation and then concentrating the medium using selected cartridge filters. The concentrate containing PRO may further be purified using selected column chromatography resins.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 9: Expression of PRO in Baculovirus-Infected Insect Cells

The following method describes recombinant expression of PRO in Baculovirus-infected insect cells.

The sequence coding for PRO is fused upstream of an epitope tag contained within a baculovirus expression vector. Such epitope tags include poly-his tags and immunoglobulin tags (like Fc regions of IgG). A variety of plasmids may be employed, including plasmids derived from commercially available plasmids such as pVL1393 (Novagen). Briefly, the sequence encoding PRO or the desired portion of the coding sequence of PRO such as the sequence encoding the extracellular domain of a transmembrane protein or the sequence encoding the mature protein if the protein is extracellular is amplified by PCR with primers complementary to the 5' and 3' regions. The 5' primer may incorporate flanking (selected) restriction enzyme sites. The product is then digested with those selected restriction enzymes and subcloned into the expression vector.

Recombinant baculovirus is generated by co-transfecting the above plasmid and BaculoGold™ virus DNA (Pharmingen) into *Spodoptera frugiperda* ("Sf9") cells (ATCC CRL 1711) using lipofectin (commercially available from GIBCO-BRL). After 4 - 5 days of incubation at 28°C, the released viruses are harvested and used for further amplifications. Viral infection and protein expression are performed as described by O'Reilley et al., Baculovirus expression vectors: A Laboratory Manual, Oxford: Oxford University Press (1994).

Expressed poly-his tagged PRO can then be purified, for example, by $Ni^{2+}$-chelate affinity chromatography as follows. Extracts are prepared from recombinant virus-infected Sf9 cells as described by Rupert et al., Nature, 362:175-179 (1993). Briefly, Sf9 cells are washed, resuspended in sonication buffer (25 mL Hepes, pH 7.9; 12.5 mM $MgCl_2$; 0.1 mM EDTA; 10% glycerol; 0.1% NP-40; 0.4 M KCl), and sonicated twice for 20 seconds on ice. The sonicates are cleared by centrifugation, and the supernatant is diluted 50-fold in loading buffer (50 mM phosphate, 300 mM NaCl, 10% glycerol, pH 7.8) and filtered through a 0.45 $\mu$m filter. A $Ni^{2+}$-NTA agarose column (commercially available from Qiagen) is prepared with a bed volume of 5 mL, washed with 25 mL of water and equilibrated with 25 mL of loading buffer. The filtered cell extract is loaded onto the column at 0.5 mL per minute. The column is washed to baseline $A_{280}$ with loading buffer, at which point fraction collection is started. Next, the column is washed with a secondary wash buffer (50 mM phosphate; 300 mM NaCl, 10% glycerol, pH 6.0), which elutes nonspecifically bound protein. After reaching $A_{280}$ baseline again, the column is developed with a 0 to 500 mM Imidazole gradient in the secondary wash buffer. One mL fractions are collected and analyzed by SDS-PAGE and silver staining or Western blot with $Ni^{2+}$-NTA-conjugated to alkaline phosphatase (Qiagen). Fractions containing the eluted $His_{10}$-tagged PRO are pooled and dialyzed against loading buffer.

Alternatively, purification of the IgG tagged (or Fc tagged) PRO can be performed using known chromatography techniques, including for instance, Protein A or protein G column chromatography.

Many of the PRO polypeptides disclosed herein were successfully expressed as described above.

EXAMPLE 10: Preparation of Antibodies that Bind PRO

This example illustrates preparation of monoclonal antibodies which can specifically bind PRO.

Techniques for producing the monoclonal antibodies are known in the art and are described, for instance, in Goding, supra. Immunogens that may be employed include purified PRO, fusion proteins containing PRO,

and cells expressing recombinant PRO on the cell surface. Selection of the immunogen can be made by the skilled artisan without undue experimentation.

Mice, such as Balb/c, are immunized with the PRO immunogen emulsified in complete Freund's adjuvant and injected subcutaneously or intraperitoneally in an amount from 1-100 micrograms. Alternatively, the immunogen is emulsified in MPL-TDM adjuvant (Ribi Immunochemical Research, Hamilton, MT) and injected into the animal's hind foot pads. The immunized mice are then boosted 10 to 12 days later with additional immunogen emulsified in the selected adjuvant. Thereafter, for several weeks, the mice may also be boosted with additional immunization injections. Serum samples may be periodically obtained from the mice by retro-orbital bleeding for testing in ELISA assays to detect anti-PRO antibodies.

After a suitable antibody titer has been detected, the animals "positive" for antibodies can be injected with a final intravenous injection of PRO. Three to four days later, the mice are sacrificed and the spleen cells are harvested. The spleen cells are then fused (using 35% polyethylene glycol) to a selected murine myeloma cell line such as P3X63AgU.1, available from ATCC, No. CRL 1597. The fusions generate hybridoma cells which can then be plated in 96 well tissue culture plates containing HAT (hypoxanthine, aminopterin, and thymidine) medium to inhibit proliferation of non-fused cells, myeloma hybrids, and spleen cell hybrids.

The hybridoma cells will be screened in an ELISA for reactivity against PRO. Determination of "positive" hybridoma cells secreting the desired monoclonal antibodies against PRO is within the skill in the art.

The positive hybridoma cells can be injected intraperitoneally into syngeneic Balb/c mice to produce ascites containing the anti-PRO monoclonal antibodies. Alternatively, the hybridoma cells can be grown in tissue culture flasks or roller bottles. Purification of the monoclonal antibodies produced in the ascites can be accomplished using ammonium sulfate precipitation, followed by gel exclusion chromatography. Alternatively, affinity chromatography based upon binding of antibody to protein A or protein G can be employed.

EXAMPLE 11: Purification of PRO Polypeptides Using Specific Antibodies

Native or recombinant PRO polypeptides may be purified by a variety of standard techniques in the art of protein purification. For example, pro-PRO polypeptide, mature PRO polypeptide, or pre-PRO polypeptide is purified by immunoaffinity chromatography using antibodies specific for the PRO polypeptide of interest. In general, an immunoaffinity column is constructed by covalently coupling the anti-PRO polypeptide antibody to an activated chromatographic resin.

Polyclonal immunoglobulins are prepared from immune sera either by precipitation with ammonium sulfate or by purification on immobilized Protein A (Pharmacia LKB Biotechnology, Piscataway, N.J.). Likewise, monoclonal antibodies are prepared from mouse ascites fluid by ammonium sulfate precipitation or chromatography on immobilized Protein A. Partially purified immunoglobulin is covalently attached to a chromatographic resin such as CnBr-activated SEPHAROSE™ (Pharmacia LKB Biotechnology). The antibody is coupled to the resin, the resin is blocked, and the derivative resin is washed according to the manufacturer's instructions.

Such an immunoaffinity column is utilized in the purification of PRO polypeptide by preparing a fraction from cells containing PRO polypeptide in a soluble form. This preparation is derived by solubilization of the

whole cell or of a subcellular fraction obtained via differential centrifugation by the addition of detergent or by other methods well known in the art. Alternatively, soluble PRO polypeptide containing a signal sequence may be secreted in useful quantity into the medium in which the cells are grown.

A soluble PRO polypeptide-containing preparation is passed over the immunoaffinity column, and the column is washed under conditions that allow the preferential absorbance of PRO polypeptide (*e.g.*, high ionic strength buffers in the presence of detergent). Then, the column is eluted under conditions that disrupt antibody/PRO polypeptide binding (*e.g.*, a low pH buffer such as approximately pH 2-3, or a high concentration of a chaotrope such as urea or thiocyanate ion), and PRO polypeptide is collected.

EXAMPLE 12: Drug Screening

This invention is particularly useful for screening compounds by using PRO polypeptides or binding fragment thereof in any of a variety of drug screening techniques. The PRO polypeptide or fragment employed in such a test may either be free in solution, affixed to a solid support, borne on a cell surface, or located intracellularly. One method of drug screening utilizes eukaryotic or prokaryotic host cells which are stably transformed with recombinant nucleic acids expressing the PRO polypeptide or fragment. Drugs are screened against such transformed cells in competitive binding assays. Such cells, either in viable or fixed form, can be used for standard binding assays. One may measure, for example, the formation of complexes between PRO polypeptide or a fragment and the agent being tested. Alternatively, one can examine the diminution in complex formation between the PRO polypeptide and its target cell or target receptors caused by the agent being tested.

Thus, the present invention provides methods of screening for drugs or any other agents which can affect a PRO polypeptide-associated disease or disorder. These methods comprise contacting such an agent with an PRO polypeptide or fragment thereof and assaying (I) for the presence of a complex between the agent and the PRO polypeptide or fragment, or (ii) for the presence of a complex between the PRO polypeptide or fragment and the cell, by methods well known in the art. In such competitive binding assays, the PRO polypeptide or fragment is typically labeled. After suitable incubation, free PRO polypeptide or fragment is separated from that present in bound form, and the amount of free or uncomplexed label is a measure of the ability of the particular agent to bind to PRO polypeptide or to interfere with the PRO polypeptide/cell complex.

Another technique for drug screening provides high throughput screening for compounds having suitable binding affinity to a polypeptide and is described in detail in WO 84/03564, published on September 13, 1984. Briefly stated, large numbers of different small peptide test compounds are synthesized on a solid substrate, such as plastic pins or some other surface. As applied to a PRO polypeptide, the peptide test compounds are reacted with PRO polypeptide and washed. Bound PRO polypeptide is detected by methods well known in the art. Purified PRO polypeptide can also be coated directly onto plates for use in the aforementioned drug screening techniques. In addition, non-neutralizing antibodies can be used to capture the peptide and immobilize it on the solid support.

This invention also contemplates the use of competitive drug screening assays in which neutralizing antibodies capable of binding PRO polypeptide specifically compete with a test compound for binding to PRO polypeptide or fragments thereof. In this manner, the antibodies can be used to detect the presence of any peptide

which shares one or more antigenic determinants with PRO polypeptide.

EXAMPLE 13: Rational Drug Design

The goal of rational drug design is to produce structural analogs of biologically active polypeptide of interest (*i.e.*, a PRO polypeptide) or of small molecules with which they interact, *e.g.*, agonists, antagonists, or inhibitors. Any of these examples can be used to fashion drugs which are more active or stable forms of the PRO polypeptide or which enhance or interfere with the function of the PRO polypeptide *in vivo* (*c.f.*, Hodgson, Bio/Technology, 9: 19-21 (1991)).

In one approach, the three-dimensional structure of the PRO polypeptide, or of an PRO polypeptide-inhibitor complex, is determined by x-ray crystallography, by computer modeling or, most typically, by a combination of the two approaches. Both the shape and charges of the PRO polypeptide must be ascertained to elucidate the structure and to determine active site(s) of the molecule. Less often, useful information regarding the structure of the PRO polypeptide may be gained by modeling based on the structure of homologous proteins. In both cases, relevant structural information is used to design analogous PRO polypeptide-like molecules or to identify efficient inhibitors. Useful examples of rational drug design may include molecules which have improved activity or stability as shown by Braxton and Wells, Biochemistry, 31:7796-7801 (1992) or which act as inhibitors, agonists, or antagonists of native peptides as shown by Athauda *et al.*, J. Biochem., 113:742-746 (1993).

It is also possible to isolate a target-specific antibody, selected by functional assay, as described above, and then to solve its crystal structure. This approach, in principle, yields a pharmacore upon which subsequent drug design can be based. It is possible to bypass protein crystallography altogether by generating anti-idiotypic antibodies (anti-ids) to a functional, pharmacologically active antibody. As a mirror image of a mirror image, the binding site of the anti-ids would be expected to be an analog of the original receptor. The anti-id could then be used to identify and isolate peptides from banks of chemically or biologically produced peptides. The isolated peptides would then act as the pharmacore.

By virtue of the present invention, sufficient amounts of the PRO polypeptide may be made available to perform such analytical studies as X-ray crystallography. In addition, knowledge of the PRO polypeptide amino acid sequence provided herein will provide guidance to those employing computer modeling techniques in place of or in addition to x-ray crystallography.

EXAMPLE 14: Ability of PRO Polypeptides to Stimulate the Release of Proteoglycans from Cartilage (Assay 97)

The ability of various PRO polypeptides to stimulate the release of proteoglycans from cartilage tissue was tested as follows.

The metacarphophalangeal joint of 4-6 month old pigs was aseptically dissected, and articular cartilage was removed by free hand slicing being careful to avoid the underlying bone. The cartilage was minced and cultured in bulk for 24 hours in a humidified atmosphere of 95% air, 5% $CO_2$ in serum free (SF) media (DME/F12 1:1) with 0.1% BSA and 100U/ml penicillin and 100$\mu$g/ml streptomycin. After washing three times, approximately 100 mg of articular cartilage was aliquoted into micronics tubes and incubated for an additional

24 hours in the above SF media. PRO polypeptides were then added at 1% either alone or in combination with 18 ng/ml interleukin-1α, a known stimulator of proteoglycan release from cartilage tissue. The supernatant was then harvested and assayed for the amount of proteoglycans using the 1,9-dimethyl-methylene blue (DMB) colorimetric assay (Farndale and Buttle, Biochem. Biophys. Acta 883:173-177 (1985)). A positive result in this assay indicates that the test polypeptide will find use, for example, in the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis.

When various PRO polypeptides were tested in the above assay, the polypeptides demonstrated a marked ability to stimulate release of proteoglycans from cartilage tissue both basally and after stimulation with interleukin-1α and at 24 and 72 hours after treatment, thereby indicating that these PRO polypeptides are useful for stimulating proteoglycan release from cartilage tissue. As such, these PRO polypeptides are useful for the treatment of sports-related joint problems, articular cartilage defects, osteoarthritis or rheumatoid arthritis. PRO6018 polypeptide testing positive in this assay.

EXAMPLE 15: Human Microvascular Endothelial Cell Proliferation (Assay 146)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce proliferation of human microvascular endothelial cells in culture and, therefore, function as useful growth factors.

On day 0, human microvascular endothelial cells were plated in 96-well plates at 1000 cells/well per 100 microliter and incubated overnight in complete media [EBM-2 growth media, plus supplements: IGF-1; ascorbic acid; VEGF; hEGF; hFGF; hydrocortisone, gentamicin (GA-1000), and fetal bovine serum (FBS, Clonetics)]. On day 1, complete media was replaced by basal media [EBM-2 plus 1% FBS] and addition of PRO polypeptides at 1%, 0.1% and 0.01%. On day 7, an assessment of cell proliferation was performed using the ViaLight HS kit [ATP/luciferase Lumitech]. Results are expressed as % of the cell growth observed with control buffer.

The following PRO polypeptides stimulated human microvascular endothelial cell proliferation in this assay: PRO1313, PRO20080, and PRO21383.

The following PRO polypeptides inhibited human microvascular endothelial cell proliferation in this assay: PRO6071, PRO4487, and PRO6006.

EXAMPLE 16: Microarray Analysis to Detect Overexpression of PRO Polypeptides in Cancerous Tumors

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in diseased tissues as compared to their normal counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. For example, a selection of genes known to be expressed in certain disease states may be arrayed on a solid support. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (disease tissue) sample is greater than hybridization signal of a probe from a control (normal tissue) sample, the gene or genes

overexpressed in the disease tissue are identified. The implication of this result is that an overexpressed protein in a diseased tissue is useful not only as a diagnostic marker for the presence of the disease condition, but also as a therapeutic target for treatment of the disease condition.

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, cancerous tumors derived from various human tissues were studied for PRO polypeptide-encoding gene expression relative to non-cancerous human tissue in an attempt to identify those PRO polypeptides which are overexpressed in cancerous tumors. Cancerous human tumor tissue from any of a variety of different human tumors was obtained and compared to a "universal" epithelial control sample which was prepared by pooling non-cancerous human tissues of epithelial origin, including liver, kidney, and lung. mRNA isolated from the pooled tissues represents a mixture of expressed gene products from these different tissues. Microarray hybridization experiments using the pooled control samples generated a linear plot in a 2-color analysis. The slope of the line generated in a 2-color analysis was then used to normalize the ratios of (test:control detection) within each experiment. The normalized ratios from various experiments were then compared and used to identify clustering of gene expression. Thus, the pooled "universal control" sample not only allowed effective relative gene expression determinations in a simple 2-sample comparison, it also allowed multi-sample comparisons across several experiments.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from a panel of nine different tumor tissues (listed below) were used for the hybridization thereto. A value based upon the normalized ratio:experimental ratio was designated as a "cutoff ratio". Only values that were above this cutoff ratio were determined to be significant. Table 8 below shows the results of these experiments, demonstrating that various PRO polypeptides of the present invention are significantly overexpressed in various human tumor tissues, as compared to a non-cancerous human tissue control or other human tumor tissues. As described above, these data demonstrate that the PRO polypeptides of the present invention are useful not only as diagnostic markers for the presence of one or more cancerous tumors, but also serve as therapeutic targets for the treatment of those tumors.

TABLE 8

| Molecule | is overexpressed in: | as compared to normal control: |
|---|---|---|
| PRO240 | breast tumor | universal normal control |
| PRO240 | lung tumor | universal normal control |
| PRO256 | colon tumor | universal normal control |
| PRO256 | lung tumor | universal normal control |
| PRO256 | breast tumor | universal normal control |
| PRO306 | colon tumor | universal normal control |
| PRO306 | lung tumor | universal normal control |

TABLE 8 (cont')

| Molecule | is overexpressed in: | as compared to normal control: |
|---|---|---|
| PRO540 | lung tumor | universal normal control |
| PRO540 | colon tumor | universal normal control |
| PRO773 | breast tumor | universal normal control |
| PRO773 | colon tumor | universal normal control |
| PRO698 | colon tumor | universal normal control |
| PRO698 | breast tumor | universal normal control |
| PRO698 | lung tumor | universal normal control |
| PRO698 | prostate tumor | universal normal control |
| PRO698 | rectal tumor | universal normal control |
| PRO3567 | colon tumor | universal normal control |
| PRO3567 | breast tumor | universal normal control |
| PRO3567 | lung tumor | universal normal control |
| PRO826 | colon tumor | universal normal control |
| PRO826 | lung tumor | universal normal control |
| PRO826 | breast tumor | universal normal control |
| PRO826 | rectal tumor | universal normal control |
| PRO826 | liver tumor | universal normal control |
| PRO1002 | colon tumor | universal normal control |
| PRO1002 | lung tumor | universal normal control |
| PRO1068 | colon tumor | universal normal control |
| PRO1068 | breast tumor | universal normal control |
| PRO1030 | colon tumor | universal normal control |
| PRO1030 | breast tumor | universal normal control |
| PRO1030 | lung tumor | universal normal control |
| PRO1030 | prostate tumor | universal normal control |
| PRO1030 | rectal tumor | universal normal control |
| PRO4397 | colon tumor | universal normal control |
| PRO4397 | breast tumor | universal normal control |
| PRO4344 | colon tumor | universal normal control |
| PRO4344 | lung tumor | universal normal control |
| PRO4344 | rectal tumor | universal normal control |
| PRO4407 | colon tumor | universal normal control |
| PRO4407 | breast tumor | universal normal control |
| PRO4407 | lung tumor | universal normal control |
| PRO4407 | liver tumor | universal normal control |
| PRO4407 | rectal tumor | universal normal control |
| PRO4316 | colon tumor | universal normal control |
| PRO4316 | prostate tumor | universal normal control |
| PRO5775 | colon tumor | universal normal control |
| PRO6016 | colon tumor | universal normal control |

TABLE 8 (cont')

| Molecule | is overexpressed in: | as compared to normal control: |
|---|---|---|
| PRO4980 | breast tumor | universal normal control |
| PRO4980 | colon tumor | universal normal control |
| PRO4980 | lung tumor | universal normal control |
| PRO6018 | colon tumor | universal normal control |
| PRO7168 | colon tumor | universal normal control |
| PRO6000 | colon tumor | universal normal control |
| PRO6006 | colon tumor | universal normal control |
| PRO5800 | colon tumor | universal normal control |
| PRO5800 | breast tumor | universal normal control |
| PRO5800 | lung tumor | universal normal control |
| PRO5800 | rectal tumor | universal normal control |
| PRO7476 | colon tumor | universal normal control |
| PRO10268 | colon tumor | universal normal control |
| PRO6496 | colon tumor | universal normal control |
| PRO6496 | breast tumor | universal normal control |
| PRO6496 | lung tumor | universal normal control |
| PRO7422 | colon tumor | universal normal control |
| PRO7431 | colon tumor | universal normal control |
| PRO28633 | colon tumor | universal normal control |
| PRO28633 | lung tumor | universal normal control |
| PRO28633 | liver tumor | universal normal control |
| PRO21485 | colon tumor | universal normal control |
| PRO28700 | breast tumor | universal normal control |
| PRO28700 | lung tumor | universal normal control |
| PRO28700 | colon tumor | universal normal control |
| PRO34012 | colon tumor | universal normal control |
| PRO34012 | lung tumor | universal normal control |
| PRO34003 | colon tumor | universal normal control |
| PRO34003 | lung tumor | universal normal control |
| PRO34001 | colon tumor | universal normal control |
| PRO34009 | colon tumor | universal normal control |
| PRO34009 | breast tumor | universal normal control |
| PRO34009 | lung tumor | universal normal control |
| PRO34009 | rectal tumor | universal normal control |
| PRO34192 | colon tumor | universal normal control |

TABLE 8 (cont')

| Molecule | is overexpressed in: | as compared to normal control: |
|---|---|---|
| PRO34564 | colon tumor | universal normal control |
| PRO35444 | colon tumor | universal normal control |
| PRO5998 | colon tumor | universal normal control |
| PRO5998 | lung tumor | universal normal control |
| PRO5998 | kidney tumor | universal normal control |
| PRO19651 | colon tumor | universal normal control |
| PRO20221 | liver tumor | universal normal control |
| PRO21434 | liver tumor | universal normal control |

EXAMPLE 17: Fetal Hemoglobin Induction in an Erythroblastic Cell Line (Assay 107)

This assay is useful for screening PRO polypeptides for the ability to induce the switch from adult hemoglobin to fetal hemoglobin in an erythroblastic cell line. Molecules testing positive in this assay are expected to be useful for therapeutically treating various mammalian hemoglobin-associated disorders such as the various thalassemias. The assay is performed as follows. Erythroblastic cells are plated in standard growth medium at 1000 cells/well in a 96 well format. PRO polypeptides are added to the growth medium at a concentration of 0.2% or 2% and the cells are incubated for 5 days at 37°C. As a positive control, cells are treated with 100$\mu$M hemin and as a negative control, the cells are untreated. After 5 days, cell lysates are prepared and analyzed for the expression of gamma globin (a fetal marker). A positive in the assay is a gamma globin level at least 2-fold above the negative control.

PRO20080 polypeptide tested positive in this assay.

EXAMPLE 18: Microarray Analysis to Detect Overexpression of PRO Polypeptides in HUVEC Cells Treated with Growth Factors

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce angiogenesis by stimulating endothelial cell tube formation in HUVEC cells.

Nucleic acid microarrays, often containing thousands of gene sequences, are useful for identifying differentially expressed genes in tissues exposed to various stimuli (*e.g.*, growth factors) as compared to their normal, unexposed counterparts. Using nucleic acid microarrays, test and control mRNA samples from test and control tissue samples are reverse transcribed and labeled to generate cDNA probes. The cDNA probes are then hybridized to an array of nucleic acids immobilized on a solid support. The array is configured such that the sequence and position of each member of the array is known. Hybridization of a labeled probe with a particular array member indicates that the sample from which the probe was derived expresses that gene. If the hybridization signal of a probe from a test (exposed tissue) sample is greater than hybridization signal of a probe from a control (normal, unexposed tissue) sample, the gene or genes overexpressed in the exposed tissue are identified. The

implication of this result is that an overexpressed protein in an exposed tissue may be involved in the functional changes within the tissue following exposure to the stimuli (*e.g.*, tube formation).

The methodology of hybridization of nucleic acids and microarray technology is well known in the art. In the present example, the specific preparation of nucleic acids for hybridization and probes, slides, and hybridization conditions are all detailed in U.S. Provisional Patent Application Serial No. 60/193,767, filed on March 31, 2000 and which is herein incorporated by reference.

In the present example, HUVEC cells grown in either collagen gels or fibrin gels were induced to form tubes by the addition of various growth factors. Specifically, collagen gels were prepared as described previously in Yang *et al.*, *American J. Pathology*, 1999, 155(3):887-895 and Xin *et al.*,*American J. Pathology*, 2001, 158(3):1111-1120. Following gelation of the HUVEC cells, 1X basal medium containing M199 supplemented with 1%FBS, 1X ITS, 2 mM L-glutamine, 50 μg/ml ascorbic acid, 26.5 mM $NaHCO_3$, 100U/ml penicillin and 100 U/ml streptomycin was added. Tube formation was elicited by the inclusion in the culture media of either a mixture of phorbol myrsitate acetate (50 nM), vascular endothelial cell growth factor (40 ng/ml) and basic fibroblast growth factor (40 ng/ml) ("PMA growth factor mix") or hepatocyte growth factor (40 ng/ml) and vascular endothelial cell growth factor (40 ng/ml) (HGF/VEGF mix) for the indicated period of time. Fibrin Gels were prepared by suspending Huvec ($4 \times 10^5$ cells/ml) in M199 containing 1% fetal bovine serum (Hyclone) and human fibrinogen (2.5mg/ml). Thrombin (50U/ml) was then added to the fibrinogen suspension at a ratio of 1 part thrombin solution:30 parts fibrinogen suspension. The solution was then layered onto 10 cm tissue culture plates (total volume: 15 ml/plate) and allowed to solidify at 37°C for 20 min. Tissue culture media (10 ml of BM containing PMA (50 nM), bFGF (40ng/ml) and VEGF (40 ng/ml)) was then added and the cells incubated at 37°C in 5%$CO_2$ in air for the indicated period of time.

Total RNA was extracted from the HUVEC cells incubated for 0, 4, 8, 24, 40 and 50 hours in the different matrix and media combinations using a TRIzol extraction followed by a second purification using RNAeasy Mini Kit (Qiagen). The total RNA was used to prepare cRNA which was then hybridized to the microarrays.

In the present experiments, nucleic acid probes derived from the herein described PRO polypeptide-encoding nucleic acid sequences were used in the creation of the microarray and RNA from the HUVEC cells described above were used for the hybridization thereto. Pairwise comparisons were made using time 0 chips as a baseline. Three replicate samples were analyzed for each experimental condition and time. Hence there were 3 time 0 samples for each treatment and 3 replicates of each successive time point. Therefore, a 3 by 3 comparison was performed for each time point compared against each time 0 point. This resulted in 9 comparisons per time point. Only those genes that had increased expression in all three non-time-0 replicates in each of the different matrix and media combinations as compared to any of the three time zero replicates were considered positive. Although this stringent method of data analysis does allow for false negatives, it minimizes false positives.

PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933, and PRO34274 tested positive in this assay.

EXAMPLE 19: Tumor Versus Normal Differential Tissue Expression Distribution

Oligonucleotide probes were constructed from some of the PRO polypeptide-encoding nucleotide sequences shown in the accompanying figures for use in quantitative PCR amplification reactions. The oligonucleotide probes were chosen so as to give an approximately 200-600 base pair amplified fragment from the 3' end of its associated template in a standard PCR reaction. The oligonucleotide probes were employed in standard quantitative PCR amplification reactions with cDNA libraries isolated from different human tumor and normal human tissue samples and analyzed by agarose gel electrophoresis so as to obtain a quantitative determination of the level of expression of the PRO polypeptide-encoding nucleic acid in the various tumor and normal tissues tested. β-actin was used as a control to assure that equivalent amounts of nucleic acid was used in each reaction. Identification of the differential expression of the PRO polypeptide-encoding nucleic acid in one or more tumor tissues as compared to one or more normal tissues of the same tissue type renders the molecule useful diagnostically for the determination of the presence or absence of tumor in a subject suspected of possessing a tumor as well as therapeutically as a target for the treatment of a tumor in a subject possessing such a tumor. These assays provided the following results:

(1) DNA161005-2943 molecule is very highly expressed in human umblilical vein endothelial cells (HUVEC), substantia niagra, hippocampus and dendrocytes; highly expressed in lymphoblasts; expressed in spleen, prostate, uterus and macrophages; and is weakly expressed in cartilage and heart. Among a panel of normal and tumor tissues examined, it is expressed in esophageal tumor, and is not expressed in normal esophagus, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

(2) DNA170245-3053 molecule is highly expressed in cartilage, testis, adrenal gland, and uterus, and not expressed in HUVEC, colon tumor, heart, placenta, bone marrow, spleen and aortic endothelial cells. In a panel of tumor and normal tissue samples examined, the DNA170245-3053 molecule was found to be expressed in normal esophagus and esophagial tumor, expressed in normal stomach and in stomach tumor, not expressed in normal kidney, but expressed in kidney tumor, not expressed in normal lung, but expressed in lung tumor, not expressed in normal rectum nor in rectal tumor, and not expressed in normal liver, but is expressed in liver tumor.

(3) DNA173157-2981 molecule is significantly expressed in the following tissues: cartilage, testis, HUVEC, heart, placenta, bone marrow, adrenal gland, prostate, spleen, aortic endothelial cells, and uterus. When these assays were conducted on a tumor tissue panel, it was found that the DNA173157-2981 molecule is significantly expressed in the following tissues: normal esophagus and esophagial tumor, normal stomach and stomach tumor, normal kidney and kidney tumor, normal lung and lung tumor, normal rectum and rectal tumor, normal liver and liver tumor, and colon tumor.

(4) DNA175734-2985 molecule is significantly expressed in the adrenal gland and the uterus. The DNA175734-2985 molecule is not significantly expressed in the following tissues: cartilage, testis, HUVEC, colon tumor, heart, placenta, bone marrow, prostate, spleen and aortic endothelial cells. Screening of a tumor panel revealed that DNA175734-2985 is significantly expressed in normal esophagus but not in esophagial tumor. Similarly, while highly expressed in normal rectum, DNA175734-2985 is expressed to a lesser extent in rectal

tumor. DNA175734-2985 is expressed equally in normal stomach and stomach tumor as well as normal liver and liver tumor. While not expressed in normal kidney, DNA175734-2985 is highly expressed in kidney tumor.

(5) DNA176108-3040 molecule is highly expressed in prostate and uterus, expressed in cartilage, testis, heart, placenta, bone marrow, adrenal gland and spleen, and not significantly expressed in HUVEC, colon tumor, and aortic endothelial cells. In a panel of tumor and normal tissue samples examined, the DNA176108-3040 molecule was found to be highly expressed in normal esophagus, but expressed at lower levels in esophagial tumor, highly expressed in normal stomach, and expressed at a lower level in stomach tumor, expressed in kidney and in kidney tumor, expressed in normal rectum and at a lower level in rectal tumor, and expressed in normal liver and not expressed in liver tumor.

(6) DNA191064-3069 molecule is significantly expressed in the following tissues: cartilage, testis, HUVEC, heart, placenta, bone marrow, adrenal gland, prostate, spleen, aortic endothelial cells, and uterus and not significantly expressed in colon tumor. In a panel of tumor and normal tissue samples, the DNA191064-3069 molecule was found to be expressed in normal esophagus and in esophagial tumors, expressed in normal stomach and in stomach tumors, expressed in normal kidney and in kidney tumors, expressed in normal lung and in lung tumors, expressed in normal rectum and in rectal tumors, expressed in normal liver and in liver tumors.

(7) DNA194909-3013 molecule is highly expressed in placenta, and expressed in cartilage, testis, HUVEC, colon tumor, heart, bone marrow, adrenal gland, prostate, spleen, aortic endothelial cells and uterus. In a panel of tumor and normal tissue samples examined, the DNA194909-3013 molecule was found to be expressed in normal esophagus and expressed at a lower level in esophagial tumor, not expressed in normal stomach nor stomach tumor, expressed in normal kidney and kidney tumor, expressed in normal lung and lung tumor, expressed in normal rectum and rectal tumor, and not expressed in normal liver, but is expressed in liver tumor.

(8) The PRO34009 encoding genes of the invention (DNA203532-3029) were screened in normal tissues and the following primary tumors and the resulting values are reported below.

Tumor Panel:

PRO34009 encoding genes were expressed 39.3 fold higher in lung tumor than normal lung. It is expressed 9.5 fold higher in esophagial tumors than normal esophagus. It is expressed 6.7 fold higher in kidney tumor than normal kidney. It is expressed 4.0 fold higher in colon tumor than normal colon. It is expressed 2.7 fold higher in stomach tumor than normal stomach. It is expressed at similar levels in normal rectum and rectal tumor, normal liver and liver tumor, normal uterus and uterine tumor.

Normal Panel:

For the normal tissue values, the normal tissue with the highest expression, in this case normal thymus, was given a value of 1 and all other normal tissues were given a value of less than 1,and described as expressed, weakly expressed or not expressed, based on their expression relative to thymus. PRO34009 encoding genes were expressed in normal thymus. It is weakly expressed in lymphoblast, spleen, heart, fetal limb, fetal lung, placenta, HUVEC, testis, fetal kidney, uterus, prostate, macrophage, substantia nigra, hippocampus, liver, skin, esophagus, stomach, rectum, kidney, thyroid, skeletal muscle, or fetal articular cartilage.

It is not expressed in bone marrow, fetal liver, colon, lung or dendrocytes.

(9) DNA213858-3060 molecule is not significantly expressed in cartilage, testis, HUVEC, colon tumor, heart,

placenta, bone marrow, adrenal gland, prostate, spleen, aortic endothelial cells or uterus. In a panel of tumor and normal tissue samples examined, the DNA213858-3060 molecule was found to be expressed in normal esophagus and esophagial tumor, expressed in normal stomach and in stomach tumor, expressed in normal kidney and and kidney tumor, expressed in normal lung and in lung tumor, expressed in normal rectum and in rectal tumor, and expressed in normal liver and in liver tumor.

(10) DNA216676-3083 molecule is significantly expressed in the following tissues: testis, heart, bone marrow, and uterus, and not significantly expressed in the following tissues: cartilage, HUVEC, colon tumor, placenta, adrenal gland, prostate, spleen, or aortic endothelial cells In a panel of tumor and normal tissues samples examined, the DNA216676-3083 molecule was found to be expressed in normal esophagus and esophagial tumor, not expressed in normal stomach, but isexpressed in stomach tumor, not expressed in normal kidney nor in kidney tumor, not expressed in normal lung, but is expressed in lung tumor, not expressed in normal rectum, but is expressed in rectal tumor, and not expressed in normal liver nor in liver tumor.

(11) DNA222653-3104 molecule is significantly expressed testis, and not significantly expressed in cartilage, HUVEC, colon tumor, heart, placenta, bone marrow, adrenal gland, prostate, spleen, aortic endothelial cells and uterus. In a panel of tumor and normal tissue samples examined, the DNA22653-3104 molecule was not expressed in normal esophagus, esophagial tumor, normal stomach, stomach tumor, normal kidney, kidney tumor, normal lung, lung tumor, normal rectum, rectal tumor, normal liver and liver tumor.

EXAMPLE 20: Guinea Pig Vascular Leak (Assay 51)

This assay is designed to determine whether PRO polypeptides of the present invention show the ability to induce vascular permeability. Polypeptides testing positive in this assay are expected to be useful for the therapeutic treatment of conditions which would benefit from enhanced vascular permeability including, for example, conditions which may benefit from enhanced local immune system cell infiltration.

Hairless guinea pigs weighing 350 grams or more were anesthetized with Ketamine (75-80 mg/kg) and 5 mg/kg Xylazine intramuscularly. Test samples containing the PRO polypeptide or a physiological buffer without the test polypeptide are injected into skin on the back of the test animals with 100 $\mu$l per injection site intradermally. There were approximately 16-24 injection sites per animal. One ml of Evans blue dye (1% in PBS) is then injected intracardially. Skin vascular permeability responses to the compounds (*i.e.*, blemishes at the injection sites of injection) are visually scored by measuring the diameter (in mm) of blue-colored leaks from the site of injection at 1 and 6 hours post administration of the test materials. The mm diameter of blueness at the site of injection is observed and recorded as well as the severity of the vascular leakage. Blemishes of at least 5 mm in diameter are considered positive for the assay when testing purified proteins, being indicative of the ability to induce vascular leakage or permeability. A response greater than 7 mm diameter is considered positive for conditioned media samples. Human VEGF at 0.1 $\mu$g/100 $\mu$l is used as a positive control, inducing a response of 15-23 mm diameter.

PRO19822 polypeptides tested positive in this assay.

EXAMPLE 21: Skin Vascular Permeability Assay (Assay 64)

This assay shows that certain polypeptides of the invention stimulate an immune response and induce inflammation by inducing mononuclear cell, eosinophil and PMN infiltration at the site of injection of the animal. Compounds which stimulate an immune response are useful therapeutically where stimulation of an immune response is beneficial. This skin vascular permeability assay is conducted as follows. Hairless guinea pigs weighing 350 grams or more are anesthetized with ketamine (75-80 mg/Kg) and 5 mg/Kg xylazine intramuscularly (IM). A sample of purified polypeptide of the invention or a conditioned media test sample is injected intradermally onto the backs of the test animals with 100 $\mu$l per injection site. It is possible to have about 10-30, preferably about 16-24, injection sites per animal. One $\mu$l of Evans blue dye (1% in physiologic buffered saline) is injected intracardially. Blemishes at the injection sites are then measured (mm diameter) at 1 hr and 6 hr post injection. Animals were sacrificed at 6 hrs after injection. Each skin injection site is biopsied and fixed in formalin. The skins are then prepared for histopathologic evaluation. Each site is evaluated for inflammatory cell infiltration into the skin. Sites with visible inflammatory cell inflammation are scored as positive. Inflammatory cells may be neutrophilic, eosinophilic, monocytic or lymphocytic. At least a minimal perivascular infiltrate at the injection site is scored as positive, no infiltrate at the site of injection is scored as negative.

PRO19822 polypeptide tested positive in this assay.

WHAT IS CLAIMED IS:

1. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence that encodes an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) and Figure 114 (SEQ ID NO:114.

2. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figures 95A-95B (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111) and Figure 113 (SEQ ID NO:113).

3. Isolated nucleic acid having at least 80% nucleic acid sequence identity to a nucleotide sequence selected from the group consisting of the full-length coding sequence of the nucleotide sequence shown in Figure 1 (SEQ ID NO:1), Figure 3 (SEQ ID NO:3), Figure 5 (SEQ ID NO:5), Figure 7 (SEQ ID NO:7), Figure 9 (SEQ ID NO:9), Figure 11 (SEQ ID NO:11), Figure 13 (SEQ ID NO:13), Figure 15 (SEQ ID NO:15), Figure 17 (SEQ ID NO:17), Figure 19 (SEQ ID NO:19), Figure 21 (SEQ ID NO:21), Figure 23 (SEQ ID NO:23), Figure 25 (SEQ ID NO:25), Figure 27 (SEQ ID NO:27), Figure 29 (SEQ ID NO:29), Figure 31 (SEQ ID NO:31), Figure 33 (SEQ ID NO:33), Figure 35 (SEQ ID NO:35), Figure 37 (SEQ ID NO:37), Figure 39 (SEQ ID NO:39), Figure 41 (SEQ ID NO:41), Figure 43 (SEQ ID NO:43), Figure 45 (SEQ ID NO:45), Figure 47 (SEQ ID NO:47), Figure 49 (SEQ ID NO:49), Figure 51 (SEQ ID NO:51), Figure 53 (SEQ ID NO:53), Figure 55 (SEQ ID NO:55), Figure 57 (SEQ ID NO:57), Figure 59 (SEQ ID NO:59), Figure 61 (SEQ ID NO:61), Figure 63 (SEQ ID NO:63), Figure 65 (SEQ ID NO:65), Figure 67 (SEQ ID NO:67), Figure 69 (SEQ ID NO:69), Figure 71 (SEQ ID NO:71), Figure 73 (SEQ ID NO:73), Figure 75 (SEQ ID NO:75), Figure 77 (SEQ ID NO:77), Figure 79 (SEQ ID NO:79), Figure 81 (SEQ ID NO:81), Figure 83 (SEQ ID NO:83), Figure 85 (SEQ ID NO:85), Figure 87 (SEQ ID NO:87), Figure 89 (SEQ ID NO:89), Figure 91 (SEQ ID NO:91), Figure 93 (SEQ ID NO:93), Figures 95A-95B (SEQ ID NO:95), Figure 97 (SEQ ID NO:97), Figure 99 (SEQ ID NO:99), Figure 101 (SEQ ID NO:101), Figure 103 (SEQ ID NO:103), Figure 105 (SEQ ID NO:105), Figure 107 (SEQ ID NO:107), Figure 109 (SEQ ID NO:109), Figure 111 (SEQ ID NO:111) and Figure 113 (SEQ ID NO:113).

4. Isolated nucleic acid having at least 80% nucleic acid sequence identity to the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

5. A vector comprising the nucleic acid of Claim 1.

6. A host cell comprising the vector of Claim 5.

7. The host cell of Claim 6, wherein said cell is a CHO cell.

8. The host cell of Claim 6, wherein said cell is an *E. coli*.

9. The host cell of Claim 6, wherein said cell is a yeast cell.

10. A process for producing a PRO polypeptide comprising culturing the host cell of Claim 6 under conditions suitable for expression of said PRO polypeptide and recovering said PRO polypeptide from the cell culture.

11. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence selected from the group consisting of the amino acid sequence shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10),

Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) and Figure 114 (SEQ ID NO:114).

12. An isolated polypeptide having at least 80% amino acid sequence identity to an amino acid sequence encoded by the full-length coding sequence of the DNA deposited under any ATCC accession number shown in Table 7.

13. A chimeric molecule comprising a polypeptide according to Claim 11 fused to a heterologous amino acid sequence.

14. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is an epitope tag sequence.

15. The chimeric molecule of Claim 13, wherein said heterologous amino acid sequence is a Fc region of an immunoglobulin.

16. An antibody which specifically binds to a polypeptide according to Claim 11.

17. The antibody of Claim 16, wherein said antibody is a monoclonal antibody, a humanized antibody or a single-chain antibody.

18. Isolated nucleic acid having at least 80% nucleic acid sequence identity to:

(a) a nucleotide sequence encoding the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26),

Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), lacking its associated signal peptide;

(b) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), with its associated signal peptide; or

(c) a nucleotide sequence encoding an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56

(SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), lacking its associated signal peptide.

19. An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) an amino acid sequence of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), lacking its associated signal peptide;

(b) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26 (SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), with its associated signal peptide; or

(c) an amino acid sequence of an extracellular domain of the polypeptide shown in Figure 2 (SEQ ID NO:2), Figure 4 (SEQ ID NO:4), Figure 6 (SEQ ID NO:6), Figure 8 (SEQ ID NO:8), Figure 10 (SEQ ID NO:10), Figure 12 (SEQ ID NO:12), Figure 14 (SEQ ID NO:14), Figure 16 (SEQ ID NO:16), Figure 18 (SEQ ID NO:18), Figure 20 (SEQ ID NO:20), Figure 22 (SEQ ID NO:22), Figure 24 (SEQ ID NO:24), Figure 26

(SEQ ID NO:26), Figure 28 (SEQ ID NO:28), Figure 30 (SEQ ID NO:30), Figure 32 (SEQ ID NO:32), Figure 34 (SEQ ID NO:34), Figure 36 (SEQ ID NO:36), Figure 38 (SEQ ID NO:38), Figure 40 (SEQ ID NO:40), Figure 42 (SEQ ID NO:42), Figure 44 (SEQ ID NO:44), Figure 46 (SEQ ID NO:46), Figure 48 (SEQ ID NO:48), Figure 50 (SEQ ID NO:50), Figure 52 (SEQ ID NO:52), Figure 54 (SEQ ID NO:54), Figure 56 (SEQ ID NO:56), Figure 58 (SEQ ID NO:58), Figure 60 (SEQ ID NO:60), Figure 62 (SEQ ID NO:62), Figure 64 (SEQ ID NO:64), Figure 66 (SEQ ID NO:66), Figure 68 (SEQ ID NO:68), Figure 70 (SEQ ID NO:70), Figure 72 (SEQ ID NO:72), Figure 74 (SEQ ID NO:74), Figure 76 (SEQ ID NO:76), Figure 78 (SEQ ID NO:78), Figure 80 (SEQ ID NO:80), Figure 82 (SEQ ID NO:82), Figure 84 (SEQ ID NO:84), Figure 86 (SEQ ID NO:86), Figure 88 (SEQ ID NO:88), Figure 90 (SEQ ID NO:90), Figure 92 (SEQ ID NO:92), Figure 94 (SEQ ID NO:94), Figure 96 (SEQ ID NO:96), Figure 98 (SEQ ID NO:98), Figure 100 (SEQ ID NO:100), Figure 102 (SEQ ID NO:102), Figure 104 (SEQ ID NO:104), Figure 106 (SEQ ID NO:106), Figure 108 (SEQ ID NO:108), Figure 110 (SEQ ID NO:110), Figure 112 (SEQ ID NO:112) or Figure 114 (SEQ ID NO:114), lacking its associated signal peptide.

20. A method for stimulating the proliferation or differentiation of chondrocyte cells, said method comprising contacting said cells with a PRO6018 polypeptide, wherein the proliferation or differentiation of said cells is stimulated.

21. A method for stimulating the proliferation of human microvascular endothelial cells, said method comprising contacting said cells with a PRO1313, PRO20080 or PRO21383 polypeptide, wherein the proliferation of said cells is stimulated.

24. A method for inhibiting the proliferation of human microvascular endothelial cells, said method comprising contacting said cells with a PRO6071, PRO4487 or PRO6006 polypeptide, wherein the proliferation of said cells is inhibited.

25. A method for detecting the presence of tumor in a mammal, said method comprising comparing the level of expression of any PRO polypeptide shown in Table 8 in (a) a test sample of cells taken from said mammal and (b) a control sample of normal cells of the same cell type, wherein a higher level of expression of said PRO polypeptide in the test sample as compared to the control sample is indicative of the presence of tumor in said mammal.

26. The method of Claim 25, wherein said tumor is lung tumor, colon tumor, breast tumor, prostate tumor, rectal tumor, kidney tumor or liver tumor.

27. A method for inducing endothelial cell tube formation comprising administering to the endothelial cell a PRO281, PRO1560, PRO189, PRO4499, PRO6308, PRO6000, PRO10275, PRO21207, PRO20933 or

PRO34274 polypeptide, or agonist thereof, wherein tube formation in said endothelial cell is induced.

28. An oligonucleotide probe derived from any of the nucleotide sequences shown in the accompanying figures.

# FIGURE 1

CGGACGCGTGGGTGCGAGGCGAAGGTGACCGGGGACCGAGCATTTCAGATCTGCTCGGTAGA
CCTGGTGCACCACCACC**ATG**TTGGCTGCAAGGCTGGTGTGTCTCCGGACACTACCTTCTAGG
GTTTTCCACCCAGCTTTCACCAAGGCCTCCCCTGTTGTGAAGAATTCCATCACGAAGAATCA
ATGGCTGTTAACACCTAGCAGGGAATATGCCACCAAAACAAGAATTGGGATCCGGCGTGGGA
GAACTGGCCAAGAACTCAAAGAGGCAGCATTGGAACCATCGATGGAAAAAATATTTAAAATT
GATCAGATGGGAAGATGGTTTGTTGCTGGAGGGGCTGCTGTTGGTCTTGGAGCATTGTGCTA
CTATGGCTTGGGACTGTCTAATGAGATTGGAGCTATTGAAAAGGCTGTAATTTGGCCTCAGT
ATGTCAAGGATAGAATTCATTCCACCTATATGTACTTAGCAGGGAGTATTGGTTTAACAGCT
TTGTCTGCCATAGCAATCAGCAGAACGCCTGTTCTCATGAACTTCATGATGAGAGGCTCTTG
GGTGACAATTGGTGTGACCTTTGCAGCCATGGTTGGAGCTGGAATGCTGGTACGATCAATAC
CATATGACCAGAGCCCAGGCCCAAAGCATCTTGCTTGGTTGCTACATTCTGGTGTGATGGGT
GCAGTGGTGGCTCCTCTGACAATATTAGGGGGTCCTCTTCTCATCAGAGCTGCATGGTACAC
AGCTGGCATTGTGGGAGGCCTCTCCACTGTGGCCATGTGTGCGCCCAGTGAAAAGTTTCTGA
ACATGGGTGCACCCCTGGGAGTGGGCCTGGGTCTCGTCTTTGTGTCCTCATTGGGATCTATG
TTTCTTCCACCTACCACCGTGGCTGGTGCCACTCTTTACTCAGTGGCAATGTACGGTGGATT
AGTTCTTTTCAGCATGTTCCTTCTGTATGATACCCAGAAAGTAATCAAGCGTGCAGAAGTAT
CACCAATGTATGGAGTTCAAAAATATGATCCCATTAACTCGATGCTGAGTATCTACATGGAT
ACATTAAATATATTTATGCGAGTTGCAACTATGCTGGCAACTGGAGGCAACAGAAAGAAA**TG**
**A**AGTGACTCAGCTTCTGGCTTCTCTGCTACATCAAATATCTTGTTTAATGGGGCAGATATGC
ATTAAATAGTTTGTACAAGCAGCTTTCGTTGAAGTTTAGAAGATAAGAAACATGTCATCATA
TTTAAATGTTCCGGTAATGTGATGCCTCAGGTCTGCCTTTTTTTCTGGAGAATAAATGCAGT
AATCCTCTCCCAAATAAGCACACACATTTTCAATTCTCATGTTTGAGTGATTTTAAAATGTT
TTGGTGAATGTGAAAACTAAAGTTTGTGTCATGAGAATGTAAGTCTTTTTTCTACTTTAAAA
TTTAGTAGGTTCACTGAGTAACTAAAATTTAGCAAACCTGTGTTTGCATATTTTTTTGGAGT
GCAGAATATTGTAATTAATGTCATAAGTGATTTGGAGCTTTGGTAAAGGGACCAGAGAGAAG
GAGTCACCTGCAGTCTTTTGTTTTTTTAAATACTTAGAACTTAGCACTTGTGTTATTGATTA
GTGAGGAGCCAGTAAGAAACATCTGGGTATTTGGAAACAAGTGGTCATTGTTACATTCATTT
GCTGAACTTAACAAAACTGTTCATCCTGAAACAGGCACAGGTGATGCATTCTCCTGCTGTTG
CTTCTCAGTGCTCTCTTTCCAATATAGATGTGGTCATGTTTGACTTGTACAGAATGTTAATC
ATACAGAGAATCCTTGATGGAATTATATATGTGTGTTTTACTTTTGAATGTTACAAAAGGAA
ATAACTTTAAAACTATTCTCAAGAGAAAATATTCAAAGCATGAAATATGTTGCTTTTTCCAG
AATACAAACAGTATACTCATG

# FIGURE 2

MLAARLVCLRTLPSRVFHPAFTKASPVVKNSITKNQWLLTPSREYATKTRIGIRRGRTGQEL
KEAALEPSMEKIFKIDQMGRWFVAGGAAVGLGALCYYGLGLSNEIGAIEKAVIWPQYVKDRI
HSTYMYLAGSIGLTALSAIAISRTPVLMNFMMRGSWVTIGVTFAAMVGAGMLVRSIPYDQSP
GPKHLAWLLHSGVMGAVVAPLTILGGPLLIRAAWYTAGIVGGLSTVAMCAPSEKFLNMGAPL
GVGLGLVFVSSLGSMFLPPTTVAGATLYSVAMYGGLVLFSMFLLYDTQKVIKRAEVSPMYGV
QKYDPINSMLSIYMDTLNIFMRVATMLATGGNRKK

# FIGURE 3

CCAATCGCCCGGTGCGGTGGTGCAGGGTCTCGGGCTAGTCATGGCGTCCCCGTCTCGGAGACTGCAGACTAAAC
CAGTCATTACTTGTTTCAAGAGCGTTCTGCTAATCTACACTTTTATTTTCTGGATCACTGGCGTTATCCTTCTT
GCAGTTGGCATTTGGGGCAAGGTGAGCCTGGAGAATTACTTTTCTCTTTTAAATGAGAAGGCCACCAATGTCCC
CTTCGTGCTCATTGCTACTGGTACCGTCATTATTCTTTTGGGCACCTTTGGTTGTTTTGCTACCTGCCGAGCTT
CTGCATGGATGCTAAAACTGTATGCAATGTTTCTGACTCTCGTTTTTTTGGTCGAACTGGTCGCTGCCATCGTA
GGATTTGTTTTCAGACATGAGATTAAGAACAGCTTTAAGAATAATTATGAGAAGGCTTTGAAGCAGTATAACTC
TACAGGAGATTATAGAAGCCATGCAGTAGACAAGATCCAAAATACGTTGCATTGTTGTGGTGTCACCGATTATA
GAGATTGGACAGATACTAATTATTACTCAGAAAAAGGATTTCCTAAGAGTTGCTGTAAACTTGAAGATTGTACT
CCACAGAGAGATGCAGACAAAGTAAACAATGAAGGTTGTTTTATAAAGGTGATGACCATTATAGAGTCAGAAAT
GGGAGTCGTTGCAGGAATTTCCTTTGGAGTTGCTTGCTTCCAACTGATTGGAATCTTTCTCGCCTACTGCCWCT
CTCGTGCCATAACAAATAACCAGTATGAGATAGTGTAACCCAATGTATCTGTGGGCCTATTCCTCTCTACCTTT
AAGGACATTTAGGGTCCCCCCTGTGAATTAGAAAGTTGCTTGGCTGGAGAACTGACAACACTACTTACTGATAG
ACCAAAAAACTACACCAGTAGGTTGATTCAATCAAGATGTATGTAGACCTAAAACTACACCAATAGGCTGATTC
AATCAAGATCCGTGCTCGCAGTGGGCTGATTCAATCAAGATGTATGTTTGCTATGTTCTAAGTCCACCTTCTAT
CCCATTCATGTTAGATCGTTGAAACCCTGTATCCCTCTGAAACACTGGAAGAGCTAGTAAATTGTAAATGAAGT

# FIGURE 4

MASPSRRLQTKPVITCFKSVLLIYTFIFWITGVILLAVGIWGKVSLENYFSLLNEKATNVPF
VLIATGTVIILLGTFGCFATCRASAWMLKLYAMFLTLVFLVELVAAIVGFVFRHEIKNSFKN
NYEKALKQYNSTGDYRSHAVDKIQNTLHCCGVTDYRDWTDTNYYSEKGFPKSCCKLEDCTPQ
RDADKVNNEGCFIKVMTIIESEMGVVAGISFGVACFQLIGIFLAYCXSRAITNNQYEIV

**Important features of the protein:**
**Signal peptide:**
amino acids 1-42

**Transmembrane domains:**
amino acids 19-42, 61-83, 92-114, 209-230,

**N-glycosylation site.**
amino acids 134-138

**Tyrosine kinase phosphorylation site.**
amino acids 160-168, 160-169

**N-myristoylation site.**
amino acids 75-81, 78-84, 210-216, 214-220, 226-232

**Prokaryotic membrane lipoprotein lipid attachment site.**
amino acids 69-80, 211-222

# FIGURE 5

GGGGCCGCGGTCTAGGGCGGCTACGTGTGTTGCCATAGCGACCATTTTGCATTAACTGGTTG
GTAGCTTCTATCCTGGGGGCTGAGCGACTGCGGGCCAGCTCTTCCCCTACTCCCTCTCGGCT
CCTTGTGGCCCAAAGGCCTAACCGGGGTCCGGCGGTCTGGCCTAGGGATCTTCCCCGTTGCC
CCTTTGGGGCGGGATGGCTGCGGAAGAAGAAGACGAGGTGGAGTGGGTAGTGGAGAGCATCG
CGGGGTTCCTGCGAGGCCCAGACTGGTCCATCCCCATCTTGGACTTTGTGGAACAGAAATGT
GAAGTTAACTGCAAAGGAGGGCATGTGATAACTCCAGGAAGCCCAGAGCCGGTGATTTTGGT
GGCCTGTGTTCCCCTTGTTTTTGATGATGAAGAAGAAAGCAAATTGACCTATACAGAGATTC
ATCAGGAATACAAAGAACTAGTTGAAAAGCTGTTAGAAGGTTACCTCAAAGAAATTGGAATT
AATGAAGATCAATTTCAAGAAGCATGCACTTCTCCTCTTGCAAAGACCCATACATCACAGGC
CATTTTGCAACCTGTGTTGGCAGCAGAAGATTTTACTATCTTTAAAGCAATGATGGTCCAGA
AAAACATTGAAATGCAGCTGCAAGCCATTCGAATAATTCAAGAGAGAAATGGTGTATTACCT
GACTGCTTAACCGATGGCTCTGATGTGGTCAGTGACCTTGAACACGAAGAGATGAAAATCCT
GAGGGAAGTTCTTAGAAAATCAAAAGAGGAATATGACCAGGAAGAAGAAAGGAAGAGGAAAA
AACAGTTATCAGAGGCTAAAACAGAAGAGCCCACAGTGCATTCCAGTGAAGCTGCAATAATG
AATAATTCCCAAGGGGATGGTGAACATTTTGCACACCCACCCTCAGAAGTTAAAATGCATTT
TGCTAATCAGTCAATAGAACCTTTGGGAAGAAAAGTGGAAAGGTCTGAAACTTCCTCCCTCC
CACAAAAAGGCCTGAAGATTCCTGGCTTAGAGCATGCGAGCATTGAAGGACCAATAGCAAAC
TTATCAGTACTTGGAACAGAAGAACTTCGGCAACGAGAACACTATCTCAAGCAGAAGAGAGA
TAAGTTGATGTCCATGAGAAAGGATATGAGGACTAAACAGATACAAAATATGGAGCAGAAAG
GAAAACCCACTGGGGAGGTAGAGGAAATGACAGAGAAACCAGAAATGACAGCAGAGGAGAAG
CAAACATTACTAAAGAGGAGATTGCTTGCAGAGAAACTCAAAGAAGAAGTTATTAATAAGTA
ATAATTAAGAACAATTTAACAAAATGGAAGTTCAAATTGTCTTAAAAATAAATTATTTAGTC
CTTACACTG

# FIGURE 6

MAAEEEDEVEWVVESIAGFLRGPDWSIPILDFVEQKCEVNCKGGHVITPGSPEPVILVACVP
LVFDDEEESKLTYTEIHQEYKELVEKLLEGYLKEIGINEDQFQEACTSPLAKTHTSQAILQP
VLAAEDFTIFKAMMVQKNIEMQLQAIRIIQERNGVLPDCLTDGSDVVSDLEHEEMKILREVL
RKSKEEYDQEEERKRKKQLSEAKTEEPTVHSSEAAIMNNSQGDGEHFAHPPSEVKMHFANQS
IEPLGRKVERSETSSLPQKGLKIPGLEHASIEGPIANLSVLGTEELRQREHYLKQKRDKLMS
MRKDMRTKQIQNMEQKGKPTGEVEEMTEKPEMTAEEKQTLLKRRLLAEKLKEEVINK

**N-glycosylation sites.**
amino acids 224-228, 246-250, 285-289

**N-myristoylation site.**
amino acids 273-279

**Amidation site.**
amino acids 252-256

**Cytosolic fatty-acid binding proteins.**
amino acids 78-108

# FIGURE 7

GGGAACGGAAAATGGCGCCTCACGGCCCGGGTAGTCTTACGACCCTGGTGCCCTGGGCTGCCGCCCTGCTCCTC
GCTCTGGGCGTGGAAAGGGCTCTGGCGCTACCCGAGATATGCACCCAATGTCCAGGGAGCGTGCAAAATTTGTC
AAAAGTGGCCTTTTATTGTAAAACGACACGAGAGCTAATGCTGCATGCCCGTTGCTGCCTGAATCAGAAGGGCA
CCATCTTGGGGCTGGATCTCCAGAACTGTTCTCTGGAGGACCCTGGTCCAAACTTTCATCAGGCACATACCACT
GTCATCATAGACCTGCAAGCAAACCCCCTCAAAGGTGACTTGGCCAACACCTTCCGTGGCTTTACTCAGCTCCA
GACTCTGATACTGCCACAACATGTCAACTGTCCTGGAGGAATTAATGCCTGGAATACTATCACCTCTTATATAG
ACAACCAAATCTGTCAAGGGCAAAAGAACCTTTGCAATAACACTGGGGACCCAGAAATGTGTCCTGAGAATGGA
TCTTGTGTACCTGATGGTCCAGGTCTTTTGCAGTGTGTTTGTGCTGATGGTTTCCATGGATACAAGTGTATGCG
CCAGGGCTCGTTCTCACTGCTTATGTTCTTCGGGATTCTGGGAGCCACCACTCTATCCGTCTCCATTCTGCTTT
GGGCGACCCAGCGCCGAAAAGCCAAGACTTCATGAACTACATAGGTCTTACCATTGACCTAAGATCAATCTGAA
CTATCTTAGCCCAGTCAGGGAGCTCTGCTTCCTAGAAAGGCATCTTTCGCCAGTGGATTCGCCTCAAGGTTGAG
GCCGCCATTGGAAGATGAAAAATTGCACTCCCTTGGTGTAGACAAATACCAGTTCCCATTGGTGTTGTTGCCTA
TAATAAACACTTTTTCTTTTTTNAAAAAAAAAAAAAAAAAAAA

# FIGURE 8

**Signal Peptide:**
Amino acids 1-30

**Transmembrane:**
Amino acids 198-212

MAPHGPGSLTTLVPWAAALLLALGVERALALPEICTQCPGSVQNLSKVAFYCKTTRELMLHA
RCCLNQKGTILGLDLQNCSLEDPGPNFHQAHTTVIIDLQANPLKGDLANTFRGFTQLQTLIL
PQHVNCPGGINAWNTITSYIDNQICQGQKNLCNNTGDPEMCPENGSCVPDGPGLLQCVCADG
FHGYKCMRQGSFSLLMFFGILGATTLSVSILLWATQRRKAKTS

# FIGURE 9

GGGGGAGAAGGCGGCCGAGCCCCAGCTCTCCGAGCACCGGGTCGGAAGCCGCGACCCGAGCC
GCGCAGGAAGCTGGGACCGGAACCTCGGCGGACCCGGCCCCACCCAACTCACCTGCGCAGGT
CACCAGCACCCTCGGAACCCAGAGGCCCGCGCTCTGAAGGTGACCCCCCTGGGGAGGAAGGC
GATGGCCCCTGCGAGGACGATGGCCCGCGCCCGCCTCGCCCCGGCCGGCATCCCTGCCGTCG
CCTTGTGGCTTCTGTGCACGCTCGGCCTCCAGGGCACCCAGGCCGGGCCACCGCCCGCGCCC
CCTGGGCTGCCCGCGGGAGCCGACTGCCTGAACAGCTTTACCGCCGGGGTGCCTGGCTTCGT
GCTGGACACCAACGCCTCGGTCAGCAACGGAGCTACCTTCCTGGAGTCCCCCACCGTGCGCC
GGGGCTGGGACTGCGTGCGCGCCTGCTGCACCACCCAGAACTGCAACTTGGCGCTAGTGGAG
CTGCAGCCCGACCGCGGGGAGGACGCCATCGCCGCCTGCTTCCTCATCAACTGCCTCTACGA
GCAGAACTTCGTGTGCAAGTTCGCGCCCAGGGAGGGCTTCATCAACTACCTCACGAGGGAAG
TGTACCGCTCCTACCGCCAGCTGCGGACCCAGGGCTTTGGAGGGTCTGGGATCCCCAAGGCC
TGGGCAGGCATAGACTTGAAGGTACAACCCCAGGAACCCCTGGTGCTGAAGGATGTGGAAAA
CACAGATTGGCGCCTACTGCGGGGTGACACGGATGTCAGGGTAGAGAGGAAAGACCCAAACC
AGGTGGAACTGTGGGGACTCAAGGAAGGCACCTACCTGTTCCAGCTGACAGTGACTAGCTCA
GACCACCCAGAGGACACGGCCAACGTCACAGTCACTGTGCTGTCCACCAAGCAGACAGAAGA
CTACTGCCTCGCATCCAACAAGGTGGGTCGCTGCCGGGGCTCTTTCCCACGCTGGTACTATG
ACCCCACGGAGCAGATCTGCAAGAGTTTCGTTTATGGAGGCTGCTTGGGCAACAAGAACAAC
TACCTTCGGGAAGAAGAGTGCATTCTAGCCTGTCGGGGTGTGCAAGGTGGGCCTTTGAGAGG
CAGCTCTGGGGCTCAGGCGACTTTCCCCCAGGGCCCCTCCATGGAAAGGCGCCATCCAGTGT
GCTCTGGCACCTGTCAGCCCACCCAGTTCCGCTGCAGCAATGGCTGCTGCATCGACAGTTTC
CTGGAGTGTGACGACACCCCCAACTGCCCCGACGCCTCCGACGAGGCTGCCTGTGAAAAATA
CACGAGTGGCTTTGACGAGCTCCAGCGCATCCATTTCCCCAGTGACAAAGGGCACTGCGTGG
ACCTGCCAGACACAGGACTCTGCAAGGAGAGCATCCCGCGCTGGTACTACAACCCCTTCAGC
GAACACTGCGCCCGCTTTACCTATGGTGGTTGTTATGGCAACAAGAACAACTTTGAGGAAGA
GCAGCAGTGCCTCGAGTCTTGTCGCGGCATCTCCAAGAAGGATGTGTTTGGCCTGAGGCGGG
AAATCCCCATTCCCAGCACAGGCTCTGTGGAGATGGCTGTCACAGTGTTCCTGGTCATCTGC
ATTGTGGTGGTGGTAGCCATCTTGGGTTACTGCTTCTTCAAGAACCAGAGAAAGGACTTCCA
CGGACACCACCACCACCCACCACCCACCCCTGCCAGCTCCACTGTCTCCACTACCGAGGACA
CGGAGCACCTGGTCTATAACCACACCACCCGGCCCCTCTGAGCCTGGGTCTCACCGGCTCTC
ACCTGGCCCTGCTTCCTGCTTGCCAAGGCAGAGGCCTGGGCTGGGAAAAACTTTGGAACCAG
ACTCTTGCCTGTTTCCCAGGCCCACTGTGCCTCAGAGACCAGGGCTCCAGCCCCTCTTGGAG
AAGTCTCAGCTAAGCTCACGTCCTGAGAAAGCTCAAAGGTTTGGAAGGAGCAGAAAACCCTT
GGGCCAGAAGTACCAGACTAGATGGACCTGCCTGCATAGGAGTTTGGAGGAAGTTGGAGTTT
TGTTTCCTCTGTTCAAAGCTGCCTGTCCCTACCCCATGGTGCTAGGAAGAGGAGTGGGGTGG
TGTCAGACCCTGGAGGCCCCAACCCTGTCCTCCCGAGCTCCTCTTCCATGCTGTGCGCCCAG
GGCTGGGAGGAAGGACTTCCCTGTGTAGTTTGTGCTGTAAAGAGTTGCTTTTTGTTTATTTA
ATGCTGTGGCATGGGTGAAGAGGAGGGGAAGAGGCCTGTTTGGCCTCTCTGTCCTCTCTTCC
TCTTCCCCCAAGATTGAGCTCTCTGCCCTTGATCAGCCCCACCCTGGCCTAGACCAGCAGAC
AGAGCCAGGAGAGGCTCAGCTGCATTCCGCAGCCCCCACCCCCAAGGTTCTCCAACATCACA
GCCCAGCCCACCCACTGGGTAATAAAAGTGGTTTGTGGAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 10

MAPARTMARARLAPAGIPAVALWLLCTLGLQGTQAGPPPAPPGLPAGADCLNSFTAGVPGFV
LDTNASVSNGATFLESPTVRRGWDCVRACCTTQNCNLALVELQPDRGEDAIAACFLINCLYE
QNFVCKFAPREGFINYLTREVYRSYRQLRTQGFGGSGIPKAWAGIDLKVQPQEPLVLKDVEN
TDWRLLRGDTDVRVERKDPNQVELWGLKEGTYLFQLTVTSSDHPEDTANVTVTVLSTKQTED
YCLASNKVGRCRGSFPRWYYDPTEQICKSFVYGGCLGNKNNYLREEECILACRGVQGGPLRG
SSGAQATFPQGPSMERRHPVCSGTCQPTQFRCSNGCCIDSFLECDDTPNCPDASDEAACEKY
TSGFDELQRIHFPSDKGHCVDLPDTGLCKESIPRWYYNPFSEHCARFTYGGCYGNKNNFEEE
QQCLESCRGISKKDVFGLRREIPIPSTGSVEMAVTVFLVICIVVVVAILGYCFFKNQRKDFH
GHHHHPPPTPASSTVSTTEDTEHLVYNHTTRPL

**signal sequence:**
Amino acids 1-35

**transmembrane domain:**
Amino acids 466-483

**N-glycosylation sites:**
Amino acids 66-70;235-239;523-527

**N-myristoylation sites:**
Amino acids 29-35;43-49;161-167;212-218;281-287;282-288;285-291;
310-316;313-319;422-428;423-429;426-432

**Cell attachment sequence:**
Amino acids 193-199

**Pancreatic trypsin inhibitor (Kunitz) family signatures:**
Amino acids 278-298;419-438

# FIGURE 11

GTGCTGGGCTTTTTCAGACAAGTGCATCTCCTAACCAGGTCACATTTCAGCCGCGACCCACTCTCCGCCAGTCA
CCGGAGGCAGACCGCGGGAGGAGAGCTGAGGACAGCCGCGTGCGCTTCGCCAGCAGCGGGGTGGGAGGAAGGAC
ATTAAAATACTGCAGAAGTCAAGACCCCCCCAGGTCGAACCCAGACCACG**ATG**CGCGCCCCGGGCTGCGGGCGG
CTGGTGCTGCCGCTGCTGCTCCTGGCCGCGGCAGCCCTGGCCGAAGGCGACGCCAAGGGGCTCAAGGAGGGCGA
GACCCCCGGCAATTTCATGGAGGACGAGCAATGGCTGTCGTCCATCTCGCAGTACAGCGGCAAGATCAAGCACT
GGAACCGCTTCCGAGACGAAGTGGAGGATGACTATATCAAGAGCTGGGAGGACAATCAGCAAGGAGATGAAGCC
CTGGATACCACCAAGGACCCCTGCCAGAAGGTGAAGTGCAGCCGCCACAAGGTGTGCATTGCCCAGGGCTACCA
GCGGGCCATGTGCATCAGTCGCAAGAAGCTGGAGCACAGGATCAAGCAGCCGACCGTGAAACTCCATGGAAACA
AAGACTCCATCTGCAAGCCCTGCCACATGGCCCAGCTTGCCTCTGTCTGCGGCTCAGATGGCCACACTTACAGC
TCTGTGTGTAAGCTGGAGCAACAGGCGTGCCTGAGCAGCAAGCAGCTGGCGGTGCGATGCGAGGGCCCCTGCCC
CTGCCCCACGGAGCAGGCTGCCACCTCCACCGCCGATGGCAAACCAGAGACTTGCACCGGTCAGGACCTGGCTG
ACCTGGGAGATCGGCTGCGGGACTGGTTCCAGCTCCTTCATGAGAACTCCAAGCAGAATGGCTCAGCCAGCAGT
GTAGCCGGCCCGGCCAGCGGGCTGGACAAGAGCCTGGGGGCCAGCTGCAAGGACTCCATTGGCTGGATGTTCTC
CAAGCTGGACACCAGTGCTGACCTCTTCCTGGACCAGACGGAGCTGGCCGCCATCAACCTGGACAAGTACGAGG
TCTGCATCCGTCCCTTCTTCAACTCCTGTGACACCTACAAGGATGGCCGGGTCTCTACTGCTGAGTGGTGCTTC
TGCTTCTGGAGGGAGAAGCCCCCCTGCCTGGCAGAGCTGGAGCGCATCCAGATCCAGGAGGCCGCCAAGAAGAA
GCCAGGCATCTTCATCCCGAGCTGCGACGAGGATGGCTACTACCGGAAGATGCAGTGTGACCAGAGCAGCGGTG
ACTGCTGGCGTGTGGACCAGCTGGGCCTGGAGCTGACTGGCACGCGCACGCATGGGAGCCCCGACTGCGATGAC
ATCGTGGGCTTCTCGGGGGACTTTGGAAGCGGTGTCGGCTGGGAGGATGAGGAGGAGAAGGAGACGGAGGAAGC
AGGCGAGGAGGCCGAGGAGGAGGAGGGCGAGGCAGGCGAGGCTGACGACGGGGGCTACATCTGG**TAG**ACGCCCT
CAGGAGCCGGCTGCCGGGGGGGACTCAACAGCAGAGCTCTGAGCAGCAGCAGGCAACTTCGAGAACGGATCCAG
AAATGCAGTCAGAAGGACCCTGCTCCACCTGGGGGGACTGGGAGTGTGAGTGTGCATGGCATGTGTGTGGCACA
GATGGCTGGGACGGGTGACAGTGTGAGTGCATGTGTGCATGCATGTGTGTATGTGTGTGTGTGTGGCATGCG
CTGACAAATGTGTCCTTGATCCACACTGCTCCTGGCAGAGTGAGTCACCCAAAGGCCCCTTCGGCCTCCTTGTA
GCTGTTTTCTTTCCTTTTGTTGTTGGTTTTAAAATACATTCACACACAAATACAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 12

MRAPGCGRLVLPLLLLAAAALAEGDAKGLKEGETPGNFMEDEQWLSSISQYSGKIKHWNRFRDEVEDDYIKSWE
DNQQGDEALDTTKDPCQKVKCSRHKVCIAQGYQRAMCISRKKLEHRIKQPTVKLHGNKDSICKPCHMAQLASVC
GSDGHTYSSVCKLEQQACLSSKQLAVRCEGPCPCPTEQAATSTADGKPETCTGQDLADLGDRLRDWFQLLHENS
KQNGSASSVAGPASGLDKSLGASCKDSIGWMFSKLDTSADLFLDQTELAAINLDKYEVCIRPFFNSCDTYKDGR
VSTAEWCFCFWREKPPCLAELERIQIQEAAKKKPGIFIPSCDEDGYYRKMQCDQSSGDCWRVDQLGLELTGTRT
HGSPDCDDIVGFSGDFGSGVGWEDEEEKETEEAGEEAEEEEGEAGEADDGGYIW

# FIGURE 13

TGCGGCGACCGTCGTACACC**ATG**GGCCTCCACCTCCGCCCCTACCGTGTGGGGCTGCTCCCG
GATGGCCTCCTGTTCCTCTTGCTGCTGCTAATGCTGCTCGCGGACCCAGCGCTCCCGGCCGG
ACGTCACCCCCCAGTGGTGCTGGTCCCTGGTGATTTGGGTAACCAACTGGAAGCCAAGCTGG
ACAAGCCGACAGTGGTGCACTACCTCTGCTCCAAGAAGACCGAAAGCTACTTCACAATCTGG
CTGAACCTGGAACTGCTGCTGCCTGTCATCATTGACTGCTGGATTGACAATATCAGGCTGGT
TTACAACAAAACATCCAGGGCCACCCAGTTTCCTGATGGTGTGGATGTACGTGTCCCTGGCT
TTGGGAAGACCTTCTCACTGGAGTTCCTGGACCCCAGCAAAAGCAGCGTGGGTTCCTATTTC
CACACCATGGTGGAGAGCCTTGTGGGCTGGGGCTACACACGGGGTGAGGATGTCCGAGGGGC
TCCCTATGACTGGCGCCGAGCCCCAAATGAAAACGGGCCCTACTTCCTGGCCCTCCGCGAGA
TGATCGAGGAGATGTACCAGCTGTATGGGGGCCCCGTGGTGCTGGTTGCCCACAGTATGGGC
AACATGTACACGCTCTACTTTCTGCAGCGGCAGCCGCAGGCCTGGAAGGACAAGTATATCCG
GGCCTTCGTGTCACTGGGTGCGCCCTGGGGGGGCGTGGCCAAGACCCTGCGCGTCCTGGCTT
CAGGAGACAACAACCGGATCCCAGTCATCGGGCCCCTGAAGATCCGGGAGCAGCAGCGGTCA
GCTGTCTCCACCAGCTGGCTGCTGCCCTACAACTACACATGGTCACCTGAGAAGGTGTTCGT
GCAGACACCCACAATCAACTACACACTGCGGGACTACCGCAAGTTCTTCCAGGACATCGGCT
TTGAAGATGGCTGGCTCATGCGGCAGGACACAGAAGGGCTGGTGGAAGCCACGATGCCACCT
GGCGTGCAGCTGCACTGCCTCTATGGTACTGGCGTCCCCACACCAGACTCCTTCTACTATGA
GAGCTTCCCTGACCGTGACCCTAAAATCTGCTTTGGTGACGGCGATGGTACTGTGAACTTGA
AGAGTGCCCTGCAGTGCCAGGCCTGGCAGAGCCGCCAGGAGCACCAAGTGTTGCTGCAGGAG
CTGCCAGGCAGCGAGCACATCGAGATGCTGGCCAACGCCACCACCCTGGCCTATCTGAAACG
TGTGCTCCTTGGGCCC**TGA**CTCCTGTGCCACAGGACTCCTGTGGCTCGGCCGTGGACCTGCT
GTTGGCCTCTGGGGCTGTCATGGCCCACGCGTTTTGCAAAGTTTGTGACTCACCATTCAAGG
CCCCGAGTCTTGGACTGTGAAGCATCTGCCATGGGGAAGTGCTGTTTGTTATCCTTTCTCTG
TGGCAGTGAAGAAGGAAGAAATGAGAGTCTAGACTCAAGGGACACTGGATGGCAAGAATGCT
GCTGATGGTGGAACTGCTGTGACCTTAGGACTGGCTCCACAGGGTGGACTGGCTGGGCCCTG
GTCCCAGTCCCTGCCTGGGGCCATGTGTCCCCCTATTCCTGTGGGCTTTTCATACTTGCCTA
CTGGGCCCTGGCCCCGCAGCCTTCCTATGAGGGATGTTACTGGGCTGTGGTCCTGTACCCAG
AGGTCCCAGGGATCGGCTCCTGGCCCCTCGGGTGACCCTTCCCACACACCAGCCACAGATAG
GCCTGCCACTGGTCATGGGTAGCTAGAGCTGCTGGCTTCCCTGTGGCTTAGCTGGTGGCCAG
CCTGACTGGCTTCCTGGGCGAGCCTAGTAGCTCCTGCAGGCAGGGGCAGTTTGTTGCGTTCT
TCGTGGTTCCCAGGCCCTGGGACATCTCACTCCACTCCTACCTCCCTTACCACCAGGAGCAT
TCAAGCTCTGGATTGGGCAGCAGATGTGCCCCCAGTCCCGCAGGCTGTGTTCCAGGGGCCCT
GATTTCCTCGGATGTGCTATTGGCCCCAGGACTGAAGCTGCCTCCCTTCACCCTGGGACTGT
GGTTCCAAGGATGAGAGCAGGGGTTGGAGCCATGGCCTTCTGGGAACCTATGGAGAAAGGGA
ATCCAAGGAAGCAGCCAAGGCTGCTCGCAGCTTCCCTGAGCTGCACCTCTTGCTAACCCCAC
CATCACACTGCCACCCTGCCCTAGGGTCTCACTAGTACCAAGTGGGTCAGCACAGGGCTGAG
GATGGGGCTCCTATCCACCCTGGCCAGCACCCAGCTTAGTGCTGGGACTAGCCCAGAAACTT
GAATGGGACCCTGAGAGAGCCAGGGGTCCCCTGAGGCCCCCCTAGGGGCTTTCTGTCTGCCC
CAGGGTGCTCCATGGATCTCCCTGTGGCAGCAGGCATGGAGAGTCAGGGCTGCCTTCATGGC
AGTAGGCTCTAAGTGGGTGACTGGCCACAGGCCGAGAAAAGGGTACAGCCTCTAGGTGGGGT
TCCCAAAGACGCCTTCAGGCTGGACTGAGCTGCTCTCCCACAGGGTTTCTGTGCAGCTGGAT
TTTCTCTGTTGCATACATGCCTGGCATCTGTCTCCCCTTGTTCCTGAGTGGCCCCACATGGG
GCTCTGAGCAGGCTGTATCTGGATTCTGGCAATAAAAGTACTCTGGATGCTGTAAAAAAAAA
AAAAAAAAAAAAAA

# FIGURE 14

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA44189
><subunit 1 of 1, 412 aa, 1 stop
><MW: 46658, pI: 6.65, NX(S/T): 4
MGLHLRPYRVGLLPDGLLFLLLLLMLLADPALPAGRHPPVVLVPGDLGNQLEAKLDKPTV
VHYLCSKKTESYFTIWLNLELLLPVIIDCWIDNIRLVYNKTSRATQFPDGVDVRVPGFGK
TFSLEFLDPSKSSVGSYFHTMVESLVGWGYTRGEDVRGAPYDWRRAPNENGPYFLALREM
IEEMYQLYGGPVVLVAHSMGNMYTLYFLQRQPQAWKDKYIRAFVSLGAPWGGVAKTLRVL
ASGDNNRIPVIGPLKIREQQRSAVSTSWLLPYNYTWSPEKVFVQTPTINYTLRDYRKFFQ
DIGFEDGWLMRQDTEGLVEATMPPGVQLHCLYGTGVPTPDSFYYESFPDRDPKICFGDGD
GTVNLKSALQCQAWQSRQEHQVLLQELPGSEHIEMLANATTLAYLKRVLLGP

**Signal peptide:**
Amino acids 1-28

**Potential lipid substrate binding site:**
Amino acids 147-164

**N-glycosylation sites:**
Amino acids 99-103;273-277;289-293;398-402

**Lipases, serine proteins family:**
Amino acids 189-202

**Beta-transducin family Trp-Asp repeat:**
Amino acids 353-366

**Tyrosine kinase phosphorylation site:**
Amino acids 165-174;178-186

**N-myristoylation sites:**
Amino acids 200-206;227-233;232-238;316-322

# FIGURE 15

CAGAGCAGATA**ATG**GCAAGCATGGCTGCCGTGCTCACCTGGGCTCTGGCTCTTCTTTCAGCG
TTTTCGGCCACCCAGGCACGGAAAGGCTTCTGGGACTACTTCAGCCAGACCAGCGGGGACAA
AGGCAGGGTGGAGCAGATCCATCAGCAGAAGATGGCTCGCGAGCCCGCGACCCTGAAAGACA
GCCTTGAGCAAGACCTCAACAATATGAACAAGTTCCTGGAAAAGCTGAGGCCTCTGAGTGGG
AGCGAGGCTCCTCGGCTCCCACAGGACCCGGTGGGCATGCGGCGGCAGCTGCAGGAGGAGTTG
GAGGAGGTGAAGGCTCGCCTCCAGCCCTACATGGCAGAGGCGCACGAGCTGGTGGGCTGGAA
TTTGGAGGGCTTGCGGCAGCAACTGAAGCCCTACACGATGGATCTGATGGAGCAGGTGGCCC
TGCGCGTGCAGGAGCTGCAGGAGCAGTTGCGCGTGGTGGGGGAAGACACCAAGGCCCAGTTG
CTGGGGGGCGTGGACGAGGCTTGGGCTTTGCTGCAGGGACTGCAGAGCCGCGTGGTGCACCA
CACCGGCCGCTTCAAAGAGCTCTTCCACCCATACGCCGAGAGCCTGGTGAGCGGCATCGGGC
GCCACGTGCAGGAGCTGCACCGCAGTGTGGCTCCGCACGCCCCCGCCAGCCCCGCGCGCCTC
AGTCGCTGCGTGCAGGTGCTCTCCCGGAAGCTCACGCTCAAGGCCAAGGCCCTGCACGCACG
CATCCAGCAGAACCTGGACCAGCTGCGCGAAGAGCTCAGCAGAGCCTTTGCAGGCACTGGGA
CTGAGGAAGGGGCCGGCCCGGACCCC**TAG**ATGCTCTCCGAGGAGGTGCGCCAGCGACTTCAG
GCTTTCCGCCAGGACACCTACCTGCAGATAGCTGCCTTCACTCGCGCCATCGACCAGGAGAC
TGAGGAGGTCCAGCAGCAGCTGGCGCCACCTCCACCAGGCCACAGTGCCTTCGCCCCAGAGT
TTCAACAAACAGACAGTGGCAAGGTTCTGAGCAAGCTGCAGGCCCGTCTGGATGACCTGTGG
GAAGACATCACTCACAGCCTTCATGACCAGGGCCACAGCCATCTGGGGGACCCCTGAGGATC
TACCTGCCCAGGCCCATTCCCAGCTTCTTGTCTGGGGAGCCTTGGCTCTGAGCCTCTAGCAT
GGTTCAGTCCTTGAAAGTGGCCTGTTGGGTGGAGGGTGGAAGGTCCTGTGCAGGACAGGGAG
GCCACCAAAGGGGCTGCTGTCTCCTGCATATCCAGCCTCCTGCGACTCCCCAATCTGGATGC
ATTACATTCACCAGGCTTTGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAA

# FIGURE 16

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48303
><subunit 1 of 1, 274 aa, 1 stop
><MW: 30754, pI: 7.77, NX(S/T): 0
MASMAAVLTWALALLSAFSATQARKGFWDYFSQTSGDKGRVEQIHQQKMAREPATLKDSL
EQDLNNMNKFLEKLRPLSGSEAPRLPQDPVGMRRQLQEELEEVKARLQPYMAEAHELVGW
NLEGLRQQLKPYTMDLMEQVALRVQELQEQLRVVGEDTKAQLLGGVDEAWALLQGLQSRV
VHHTGRFKELFHPYAESLVSGIGRHVQELHRSVAPHAPASPARLSRCVQVLSRKLTLKAK
ALHARIQQNLDQLREELSRAFAGTGTEEGAGPDP

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-23

**Glycosaminoglycan attachment site:**
Amino acids 200-204

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 233-237

**N-myristoylation sites:**
Amino acids 165-171;265-271

# FIGURE 17

CTAAGAGGACAAGATGAGGCCCGGCCTCTCATTTCTCCTAGCCCTTCTGTTCTTCCTTGGCC
AAGCTGCAGGGGATTTGGGGGATGTGGGACCTCCAATTCCCAGCCCCGGCTTCAGCTCTTTC
CCAGGTGTTGACTCCAGCTCCAGCTTCAGCTCCAGCTCCAGGTCGGGCTCCAGCTCCAGCCG
CAGCTTAGGCAGCGGAGGTTCTGTGTCCCAGTTGTTTTCCAATTTCACCGGCTCCGTGGATG
ACCGTGGGACCTGCCAGTGCTCTGTTTCCCTGCCAGACACCACCTTTCCCGTGGACAGAGTG
GAACGCTTGGAATTCACAGCTCATGTTCTTTCTCAGAAGTTTGAGAAAGAACTTTCTAAAGTG
AGGGAATATGTCCAATTAATTAGTGTGTATGAAAAGAAACTGTTAAACCTAACTGTCCGAAT
TGACATCATGGAGAAGGATACCATTTCTTACACTGAACTGGACTTCGAGCTGATCAAGGTAG
AAGTGAAGGAGATGGAAAAACTGGTCATACAGCTGAAGGAGAGTTTTGGTGGAAGCTCAGAA
ATTGTTGACCAGCTGGAGGTGGAGATAAGAAATATGACTCTCTTGGTAGAGAAGCTTGAGAC
ACTAGACAAAAACAATGTCCTTGCCATTCGCCGAGAAATCGTGGCTCTGAAGACCAAGCTGA
AAGAGTGTGAGGCCTCTAAAGATCAAAACACCCCTGTCGTCCACCCTCCTCCCACTCCAGGG
AGCTGTGGTCATGGTGGTGTGGTGAACATCAGCAAACCGTCTGTGGTTCAGCTCAACTGGAG
AGGGTTTTCTTATCTATATGGTGCTTGGGGTAGGGATTACTCTCCCCAGCATCCAAACAAAG
GACTGTATTGGGTGGCGCCATTGAATACAGATGGGAGACTGTTGGAGTATTATAGACTGTAC
AACACACTGGATGATTTGCTATTGTATATAAATGCTCGAGAGTTGCGGATCACCTATGGCCA
AGGTAGTGGTACAGCAGTTTACAACAACAACATGTACGTCAACATGTACAACACCGGGAATA
TTGCCAGAGTTAACCTGACCACCAACACGATTGCTGTGACTCAAACTCTCCCTAATGCTGCC
TATAATAACCGCTTTTCATATGCTAATGTTGCTTGGCAAGATATTGACTTTGCTGTGGATGA
GAATGGATTGTGGGTTATTTATTCAACTGAAGCCAGCACTGGTAACATGGTGATTAGTAAAC
TCAATGACACCACACTTCAGGTGCTAAACACTTGGTATACCAAGCAGTATAAACCATCTGCT
TCTAACGCCTTCATGGTATGTGGGGTTCTGTATGCCACCCGTACTATGAACACCAGAACAGA
AGAGATTTTTTACTATTATGACACAAACACAGGGAAAGAGGGCAAACTAGACATTGTAATGC
ATAAGATGCAGGAAAAAGTGCAGAGCATTAACTATAACCCTTTTGACCAGAAACTTTATGTC
TATAACGATGGTTACCTTCTGAATTATGATCTTTCTGTCTTGCAGAAGCCCCAGTAAGCTGT
TTAGGAGTTAGGGTGAAAGAGAAAATGTTTGTTGAAAAAATAGTCTTCTCCACTTACTTAGA
TATCTGCAGGGGTGTCTAAAAGTGTGTTCATTTTGCAGCAATGTTTAGGTGCATAGTTCTAC
CACACTAGAGATCTAGGACATTTGTCTTGATTTGGTGAGTTCTCTTGGGAATCATCTGCCTC
TTCAGGCGCATTTTGCAATAAAGTCTGTCTAGGGTGGGATTGTCAGAGGTCTAGGGGCACTG
TGGGCCTAGTGAAGCCTACTGTGAGGAGGCTTCACTAGAAGCCTTAAATTAGGAATTAAGGA
ACTTAAAACTCAGTATGGCGTCTAGGGATTCTTTGTACAGGAAATATTGCCCAATGACTAGT
CCTCATCCATGTAGCACCACTAATTCTTCCATGCCTGGAAGAAACCTGGGGACTTAGTTAGG
TAGATTAATATCTGGAGCTCCTCGAGGGACCAAATCTCCAACTTTTTTTTCCCCTCACTAGC
ACCTGGAATGATGCTTTGTATGTGGCAGATAAGTAAATTTGGCATGCTTATATATTCTACAT
CTGTAAAGTGCTGAGTTTTATGGAGAGAGGCCTTTTTATGCATTAAATTGTACATGGCAAATAA
ATCCCAGAAGGATCTGTAGATGAGGCACCTGCTTTTTCTTTTCTCTCATTGTCCACCTTACT
AAAAGTCAGTAGAATCTTCTACCTCATAACTTCCTTCCAAAGGCAGCTCAGAAGATTAGAAC
CAGACTTACTAACCAATTCCACCCCCCACCAACCCCCTTCTACTGCCTACTTTAAAAAAATT
AATAGTTTTCTATGGAACTGATCTAAGATTAGAAAAATTAATTTTCTTTAATTTCATTATGG
ACTTTTATTTACATGACTCTAAGACTATAAGAAAATCTGATGGCAGTGACAAAGTGCTAGCA
TTTATTGTTATCTAATAAAGACCTTGGAGCATATGTGCAACTTATGAGTGTATCAGTTGTTG
CATGTAATTTTTGCCTTTGTTTAAGCCTGGAACTTGTAAGAAAATGAAAATTTAATTTTTTT
TTCTAGGACGAGCTATAGAAAAGCTATTGAGAGTATCTAGTTAATCAGTGCAGTAGTTGGAA
ACCTTGCTGGTGTATGTGATGTGCTTCTGTGCTTTTGAATGACTTTATCATCTAGTCTTTGT
CTATTTTTCCTTTGATGTTCAAGTCCTAGTCTATAGGATTGGCAGTTTAAATGCTTTACTCC
CCCTTTTAAAATAAATGATTAAAATGTGCTTTGAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 18

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA48320
<subunit 1 of 1, 510 aa, 1 stop
<MW: 57280, pI: 5.61, NX(S/T): 6
MRPGLSFLLALLFFLGQAAGDLGDVGPPIPSPGFSSFPGVDSSSSFSSSSRSGSSSSRSL
GSGGSVSQLFSNFTGSVDDRGTCQCSVSLPDTTFPVDRVERLEFTAHVLSQKFEKELSKV
REYVQLISVYEKKLLNLTVRIDIMEKDTISYTELDFELIKVEVKEMEKLVIQLKESFGGS
SEIVDQLEVEIRNMTLLVEKLETLDKNNVLAIRREIVALKTKLKECEASKDQNTPVVHPP
PTPGSCGHGGVVNISKPSVVQLNWRGFSYLYGAWGRDYSPQHPNKGLYWVAPLNTDGRLL
EYYRLYNTLDDLLLYINARELRITYGQGSGTAVYNNNMYVNMYNTGNIARVNLTTNTIAV
TQTLPNAAYNNRFSYANVAWQDIDFAVDENGLWVIYSTEASTGNMVISKLNDTTLQVLNT
WYTKQYKPSASNAFMVCGVLYATRTMNTRTEEIFYYYDTNTGKEGKLDIVMHKMQEKVQS
INYNPFDQKLYVYNDGYLLNYDLSVLQKPQ

**Important features:**
**Signal peptide:**
Amino acids 1-20

**N-glycosylation sites:**
Amino acids 72-76;136-140;193-197;253-257;352-356;
411-415

**Tyrosine kinase phosphorylation site:**
Amino acids 449-457

**N-myristoylation sites:**
Amino acids 16-22;39-45;53-59;61-67;63-69;81-87;
249-255;326-332;328-334;438-444

**Legume lectins beta-chain proteins:**
Amino acids 20-40

**HBGF/FGF family proteins:**
Amino acids 338-366

# FIGURE 19

GCACCGCAGACGGCGCGGATCGCAGGGAGCCGGTCCGCCGCCGGAACGGGAGCCTGGGTGTG
CGTGTGGAGTCCGGACTCGTGGGAGACGATCGCG**ATG**AACACGGTGCTGTCGCGGGCGAACT
CACTGTTCGCCTTCTCGCTGAGCGTGATGGCGGCGCTCACCTTCGGCTGCTTCATCACCACC
GCCTTCAAAGACAGGAGCGTCCCGGTGCGGCTGCACGTCTCGCGGATCATGCTAAAAAATGT
AGAAGATTTCACTGGACCTAGAGAAAGAAGTGATCTGGGATTTATCACATTTGATATAACTG
CTGATCTAGAGAATATATTTGATTGGAATGTTAAGCAGTTGTTTCTTTATTTATCAGCAGAA
TATTCAACAAAAAATAATGCTCTGAACCAAGTTGTCCTATGGGACAAGATTGTTTTGAGAGG
TGATAATCCGAAGCTGCTGCTGAAAGATATGAAAACAAAATATTTTTTCTTTGACGATGGAA
ATGGTCTCAAGGGAAACAGGAATGTCACTTTGACCCTGTCTTGGAACGTCGTACCAAATGCT
GGAATTCTACCTCTTGTGACAGGATCAGGACACGTATCTGTCCCATTTCCAGATACATATGA
AATAACGAAGAGTTAT**TAA**ATTATTCTGAATTTGAAACAAAAA

# FIGURE 20

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA56049
><subunit 1 of 1, 180 aa, 1 stop
><MW: 20313, pI: 8.91, NX(S/T): 1
MNTVLSRANSLFAFSLSVMAALTFGCFITTAFKDRSVPVRLHVSRIMLKNVEDFTGPRER
SDLGFITFDITADLENIFDWNVKQLFLYLSAEYSTKNNALNQVVLWDKIVLRGDNPKLLL
KDMKTKYFFFDDGNGLKGNRNVTLTLSWNVVPNAGILPLVTGSGHVSVPFPDTYEITKSY

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-25

**Transmembrane domain:**
Amino acids 149-164

**N-glycosylation site:**
Amino acids 141-145

**N-myristoylation sites:**
Amino acids 25-31;135-141

**Cell attachment sequence:**
Amino acids 112-115

**TonB-dependent receptor proteins signature 1:**
Amino acids 1-21

# FIGURE 21

AAACTTGACGCCATGAAGATCCCGGTCCTTCCTGCCGTGGTGCTCCTCTCCCTCCTGGTGCT
CCACTCTGCCCAGGGAGCCACCCTGGGTGGTCCTGAGGAAGAAAGCACCATTGAGAATTATG
CGTCACGACCCGAGGCCTTTAACACCCCGTTCCTGAACATCGACAAATTGCGATCTGCGTTT
AAGGCTGATGAGTTCCTGAACTGGCACGCCCTCTTTGAGTCTATCAAAAGGAAACTTCCTTT
CCTCAACTGGGATGCCTTTCCTAAGCTGAAAGGACTGAGGAGCGCAACTCCTGATGCCCAGT
GACCATGACCTCCACTGGAAGAGGGGGCTAGCGTGAGCGCTGATTCTCAACCTACCATAACT
CTTTCCTGCCTCAGGAACTCCAATAAAACATTTTCCATCCAAA

# FIGURE 22

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA57694
><subunit 1 of 1, 99 aa, 1 stop
><MW: 11050, pI: 7.47, NX(S/T): 0
MKIPVLPAVVLLSLLVLHSAQGATLGGPEEESTIENYASRPEAFNTPFLNIDKLRSAFKA
DEFLNWHALFESIKRKLPFLNWDAFPKLKGLRSATPDAQ

**Important features:**
**Signal peptide:**
Amino acids 1-22

**N-myristoylation sites:**
Amino acids 22-28;90-96

**Homologous region to Perioxdase:**
Amino acids 16-48

# FIGURE 23

TCTCAGACTCTTGGAAGGGGCTATACTAGACACACAAAGACAGCCCCAAGAAGGACGGTGGA
GTAGTGTCCTCGCTAAAAGACAGTAGAT**ATG**CAACGCCTCTTGCTCCTGCCCTTTCTCCTGC
TGGGAACAGTTTCTGCTCTTCATCTGGAGAATGATGCCCCCCATCTGGAGAGCCTAGAGACA
CAGGCAGACCTAGGCCAGGATCTGGATAGTTCAAAGGAGCAGGAGAGAGACTTGGCTCTGAC
GGAGGAGGTGATTCAGGCAGAGGGAGAGGAGGTCAAGGCTTCTGCCTGTCAAGACAACTTTG
AGGATGAGGAAGCCATGGAGTCGGACCCAGCTGCCTTAGACAAGGACTTCCAGTGCCCCAGG
GAAGAAGACATTGTTGAAGTGCAGGGAAGTCCAAGGTGCAAGACCTGCCGCTACCTATTGGT
GCGGACTCCTAAAACTTTTGCAGAAGCTCAGAATGTCTGCAGCAGATGCTACGGAGGCAACC
TTGTCTCTATCCATGACTTCAACTTCAACTATCGCATTCAGTGCTGCACTAGCACAGTCAAC
CAAGCCCAGGTCTGGATTGGAGGCAACCTCAGGGGCTGGTTCCTGTGGAAGCGGTTTTGCTGG
ACTGATGGGAGCCACTGGAATTTTGCTTACTGGTCCCCAGGGCAACCTGGGAATGGGCAAGG
CTCCTGTGTGGCCCTATGCACCAAAGGAGGTTATTGGCGACGAGCTCAATGCGACAAGCAAC
TGCCCTTCGTCTGCTCCTTC**TAA**GCCAGCGGCACGGAGACCCTGCCAGCAGCTCCCTCCCGT
CCCCCAACCTCTCCTGCTCATAAATCCAGACTTCCCACAGCAAAAAAAAAAAAAAAAAA

# FIGURE 24

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59208
<subunit 1 of 1, 225 aa, 1 stop
<MW: 25447, pI: 4.79, NX(S/T): 0
MQRLLLLPFLLLGTVSALHLENDAPHLESLETQADLGQDLDSSKEQERDLALTEEVIQAE
GEEVKASACQDNFEDEEAMESDPAALDKDFQCPREEDIVEVQGSPRCKTCRYLLVRTPKT
FAEAQNVCSRCYGGNLVSIHDFNFNYRIQCCTSTVNQAQVWIGGNLRGWFLWKRFCWTDG
SHWNFAYWSPGQPGNGQGSCVALCTKGGYWRRAQCDKQLPFVCSF

**Important features:**
**Signal peptide:**
Amino acids 1-17

**N-myristoylation sites:**
Amino acids 13-19;103-109;134-140;164-170;
180-186;191-197;194-200;196-202;
198-204

**C-type lectin domain signature:**
Amino acids 200-224

# FIGURE 25

CAACAGAAGCCAAGAAGGAAGCCGTCTATCTTGTGGCGATC**ATG**TATAAGCTGGCCTCCTGC
TGTTTGCTTTTCACAGGATTCTTAAATCCTCTCTTATCTCTTCCTCTCCTTGACTCCAGGGA
AATATCCTTTCAACTCTCAGCACCTCATGAAGACGCGCGCTTAACTCCGGAGGAGCTAGAAA
GAGCTTCCCTTCTACAGATATTGCCAGAGATGCTGGGTGCAGAAAGAGGGGATATTCTCAGG
AAAGCAGACTCAAGTACCAACATTTTTAACCCAAGAGGAAATTTGAGAAAGTTTCAGGATTT
CTCTGGACAAGATCCTAACATTTTACTGAGTCATCTTTTGGCCAGAATCTGGAAACCATACA
AGAAACGTGAGACTCCTGATTGCTTCTGGAAATACTGTGTC**TGA**AGTGAAATAAGCATCTGT
TAGTCAGCTCAGAAACACCCATCTTAGAATATGAAAAATAACACAATGCTTGATTTGAAAAC
AGTGTGGAGAAAAACTAGGCAAACTACACCCTGTTCATTGTTACCTGGAAAATAAATCCTCT
ATGTTTTGCACAAAAAAAAAAAAAAA

# FIGURE 26

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59214
<subunit 1 of 1, 124 aa, 1 stop
<MW: 14284, pI: 8.14, NX(S/T): 0
MYKLASCCLLFTGFLNPLLSLPLLDSREISFQLSAPHEDARLTPEELERASLLQILPEML
GAERGDILRKADSSTNIFNPRGNLRKFQDFSGQDPNILLSHLLARIWKPYKKRETPDCFW
KYCV

**Important features:**
**Signal peptide:**
Amino acids 1-20

**Urotensin II signature:**
Amino acids 118-124

**Cell attachment sequence:**
Amino acids 64-67

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 112-116

**N-myristoylation sites:**
Amino acids 61-67;92-98

# FIGURE 27

CAAGTAAATGCAGCACTAGTGGGTGGGATTGAGGTATGCCCTGGTGCATAAATAGAGACTCA
GCTGTGCTGGCACACTCAGAAGCTTGGACCGCATCCTAGCCGCCGACTCACACAAGGCAGGT
GGGTGAGGAAATCCAGAGTTGCC**ATG**GAGAAAATTCCAGTGTCAGCATTCTTGCTCCTTGTG
GCCCTCTCCTACACTCTGGCCAGAGATACCACAGTCAAACCTGGAGCCAAAAAGGACACAAA
GGACTCTCGACCCAAACTGCCCCAGACCCTCTCCAGAGGTTGGGGTGACCAACTCATCTGGA
CTCAGACATATGAAGAAGCTCTATATAAATCCAAGACAAGCAACAAACCCTTGATGATTATT
CATCACTTGGATGAGTGCCCACACAGTCAAGCTTTAAAGAAAGTGTTTGCTGAAAATAAAGA
AATCCAGAAATTGGCAGAGCAGTTTGTCCTCCTCAATCTGGTTTATGAAACAACTGACAAAC
ACCTTTCTCCTGATGGCCAGTATGTCCCCAGGATTATGTTTGTTGACCCATCTCTGACAGTT
AGAGCCGATATCACTGGAAGATATTCAAATCGTCTCTATGCTTACGAACCTGCAGATACAGC
TCTGTTGCTTGACAACATGAAGAAAGCTCTCAAGTTGCTGAAGACTGAATTG**TAA**AGAAAAA
AAATCTCCAAGCCCTTCTGTCTGTCAGGCCTTGAGACTTGAAACCAGAAGAAGTGTGAGAAG
ACTGGCTAGTGTGGAAGCATAGTGAACACACTGATTAGGTTATGGTTTAATGTTACAACAAC
TATTTTTTAAGAAAAACAAGTTTTAGAAATTTGGTTTCAAGTGTACATGTGTGAAAACAATA
TTGTATACTACCATAGTGAGCCATGATTTTCTAAAAAAAAAAATAAATGTTA

# FIGURE 28

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA59485
><subunit 1 of 1, 175 aa, 1 stop
><MW: 19979, pI: 9.26, NX(S/T): 0
MEKIPVSAFLLLVALSYTLARDTTVKPGAKKDTKDSRPKLPQTLSRGWGDQLIWTQTYEE
ALYKSKTSNKPLMIIHHLDECPHSQALKKVFAENKEIQKLAEQFVLLNLVYETTDKHLSP
DGQYVPRIMFVDPSLTVRADITGRYSNRLYAYEPADTALLLDNMKKALKLLKTEL

**Important features:**
**Signal peptide:**
Amino acids 1-20

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 30-34

# FIGURE 29

AAGACCCTCTCTTTCGCTGTTTGAGAGTCTCTCGGCTCAAGGACCGGGAGGTAAGAGGTT
TGGGACTGCCCCGGCAACTCCAGGGTGTCTGGTCCACGACCTATCCTAGGCGCCATGGGT
GTGATAGGTATACAGCTGGTTGTTACCATGGTGATGGCCAGTGTCATGCAGAAGATTATA
CCTCACTATTCTCTTGCTCGATGGCTACTCTGTAATGGCAGTTTGAGGTGGTATCAACAT
CCTACAGAAGAAGAATTAAGAATTCTTGCAGGGAAACAACAAAAAGGGAAAACCAAAAAA
GATAGGAAATATAATGGTCACATTGAAAGTAAGCCATTAACCATTCCAAAGGATATTGAC
CTTCATCTAGAAACAAAGTCAGTTACAGAAGTGGATACTTTAGCATTGCATTACTTTCCA
GAATACCAGTGGCTGGTGGATTTCACAGTGGCTGCTACAGTTGTGTATCTAGTAACTGAA
GTCTACTACAATTTTATGAAGCCTACACAGGAAATGAATATCAGCTTAGTCTGGTGCCTA
CTTGTTTTGTCTTTTGCAATCAAAGTTCTATTTTCATTAACTACACACTATTTTAAAGTA
GAAGATGGTGGTGAAAGATCTGTTTGTGTCACCTTTGGATTTTTTTTCTTTGTCAAAGCA
ATGGCAGTGTTGATTGTAACAGAAAATTATCTGGAATTTGGACTTGAAACAGGGTTTACA
AATTTTTCAGACAGTGCGATGCAGTTTCTTGAAAAGCAAGGTTTAGAATCTCAGAGTCCT
GTTTCAAAACTTACTTTCAAATTTTTCCTGGCTATTTTCTGTTCATTCATTGGGGCTTTT
TTGACATTTCCTGGATTACGACTGGCTCAAATGCATCTGGATGCCCTGAATTTGGCAACA
GAAAAAATTACACAAACTTTACTTCATATCAACTTCTTGGCACCTTTATTTATGGTTTTG
CTCTGGGTAAAACCAATCACCAAAGACTACATTATGAACCCACCACTGGGCAAAGAAATT
TCCCCATCTGGAAGATGAAGATAATAGTATCTAACTCACAAGGTTATCATTGGAATAAAT
GAAAGAACACATGTAATGCAACCAGCTGGAATTAAGTGCTTAATAAATGTTCTTTTCACT
GCTTTGCCTCATCAGAATTAAAATAGAAATACTTGACTAGT

# FIGURE 30

</usr/seqdb2/sst/DNA/Dnaseqs.full/ss.DNA64966
<subunit 1 of 1, 307 aa, 1 stop
<MW: 35098, pI: 8.11, NX(S/T): 3
MGVIGIQLVVTMVMASVMQKIIPHYSLARWLLCNGSLRWYQHPTEEELRILAGKQQKGKT
KKDRKYNGHIESKPLTIPKDIDLHLETKSVTEVDTLALHYFPEYQWLVDFTVAATVVYLV
TEVYYNFMKPTQEMNISLVWCLLVLSFAIKVLFSLTTHYFKVEDGGERSVCVTFGFFFV
KAMAVLIVTENYLEFGLETGFTNFSDSAMQFLEKQGLESQSPVSKLTFKFFLAIFCSFIG
AFLTFPGLRLAQMHLDALNLATEKITQTLLHINFLAPLFMVLLWVKPITKDYIMNPPLGK
EISPSGR

**Important features:**
**Signal peptide:**
Amino acids 1-15

**Transmembrane domains:**
Amino acids 134-157;169-189;230-248;272-285

**N-glycosylation sites:**
Amino acids 34-38;135-139;203-207

**ATP/GTP-binding site motif A (P-loop):**
Amino acids 53-61

**Tyrosine kinase phosphorylation site:**
Amino acids 59-67

**N-myristoylation sites:**
Amino acids 165-171;196-202;240-246;247-253

# FIGURE 31

GTAGCATAGTGTGCAGTTCACTGGACCAAAAGCTTTGGCTGCACCTCTTCTGGAAAGCTGGCC
**ATG**GGGCTCTTCATGATCATTGCAATTCTGCTGTTCCAGAAACCCACAGTAACCGAACAACT
TAAGAAGTGCTGGAATAACTATGTACAAGGACATTGCAGGAAAATCTGCAGAGTAAATGAAG
TGCCTGAGGCACTATGTGAAAATGGGAGATACTGTTGCCTCAATATCAAGGAACTGGAAGCA
TGTAAAAAAAATTACAAAGCCACCTCGTCCAAAGCCAGCAACACTTGCACTGACTCTTCAAGA
CTATGTTACAATAATAGAAAATTTCCCAAGCCTGAAGACACAGTCTACA**TAA**ATCAAATACA
ATTTCGTTTTCACTTGCTTCTCAACCTAGTCTAATAAACTAAGGTGATGAGATATACATCTT
CTTCCTTCTGGTTTCTTGATCCTTAAAATGACCTTCGAGCATATTCTAATAAAGTGCATTGC
CAGTTAAAAAAAAAAA

# FIGURE 32

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA82403
><subunit 1 of 1, 99 aa, 1 stop
><MW: 11343, pI: 9.17, NX(S/T): 0
MGLFMIIAILLFQKPTVTEQLKKCWNNYVQGHCRKICRVNEVPEALCENGRYCCLNIKEL
EACKKITKPPRPKPATLALTLQDYVTIIENFPSLKTQST

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 64-68

# FIGURE 33

CGGACGCGTGGGCGCTGAGCCCCGGAGGCCAGGGCGTCCGGGGCTGCGCCACTTCCGAGGGC
CGAGCGCTGCCGGTCCCGGCGGTGCGACACGGCCGGGAGGAGGAGAACAACGCAAGGGGCTC
AACCGTCGGTCGCTGGAGCCCCCCCCGGGGCGTGGCCTCCCGCCCCCTCAGCTGGGGAGGGC
GGGGCTCGCTGCCCCCTGCTGCCGACTGCGACCCTTACAGGGGAGGGAGGGCGCAGGCCGCG
CGGAG**ATG**AGGAGGAGGCTGCGCCTACGCAGGGACGCATTGCTCACGCTGCTCCTTGGCGCC
TCCCTGGGCCTCTTACTCTATGCGCAGCGCGACGGCGCGGCCCCGACGGCGAGCGCGCCGCG
AGGGCGAGGGAGGGCGGCACCGAGGCCCACCCCCGGACCCCGCGCGTTCCAGTTACCCGACG
CGGGTGCAGCCCCGCCGGCCTACGAAGGGGACACACCGGCGCCGCCCACGCCTACGGGACCC
TTTGACTTCGCCCGCTATTTGCGCGCCAAGGACCAGCGGCGGTTTCCACTGCTCATTAACCA
GCCGCACAAGTGCCGCGGCGACGGCGCACCCGGTGGCCGCCCGGACCTGCTTATTGCTGTCA
AGTCGGTGGCAGAGGACTTCGAGCGGCGCCAAGCCGTGCGCCAGACGTGGGGCGCGGAGGGT
CGCGTGCAGGGGGCGCTGGTGCGCCGCGTGTTCTTGCTGGGCGTGCCCAGGGGCGCAGGCTC
GGGCGGGGCCGACGAAGTTGGGGAGGGCGCGCGAACCCACTGGCGCGCCCTGCTGCGGGCCG
AGAGCCTTGCGTATGCGGACATCCTGCTCTGGGCCTTCGACGACACCTTTTTTAACCTAACG
CTCAAGGAGATCCACTTTCTAGCCTGGGCCTCAGCTTTCTGCCCCGACGTGCGCTTCGTTTT
TAAGGGCGACGCAGATGTGTTCGTGAACGTGGGAAATCTCCTGGAGTTCCTGGCGCCGCGGGAC
CCGGCGCAAGACCTGCTTGCTGGTGACGTAATTGTGCATGCGCGGCCCATCCGCACGCGGGC
TAGCAAGTACTACATCCCCGAGGCCGTGTACGGCCTGCCCGCCTATCCGGCCTACGCGGGCG
GCGGTGGCTTTGTGCTTTCCGGGGCCACGCTGCACCGCCTGGCTGGCGCCTGTGCGCAGGTC
GAGCTCTTCCCCATCGACGACGTCTTTCTGGGCATGTGTCTGCAGCGCCTGCGGCTCACGCC
CGAGCCTCACCCTGCCTTCCGCACCTTTGGCATCCCCCAGCCTTCAGCCGCGCCGCATTTGA
GCACCTTCGACCCCTGCTTTTACCGTGAGCTGGTTGTAGTGCACGGGCTCTCGGCCGCTGAC
ATCTGGCTTATGTGGCGCCTGCTGCACGGGCCGCATGGGCCAGCCTGTGCGCATCCACAGCC
TGTCGCTGCAGGCCCCTTCCAATGGGACTCC**TAG**CTCCCCACTACAGCCCCAAGCTCCTAAC
TCAGACCCAGAATGGAGCCGGTTTCCCAGATTATTGCCGTGTATGTGGTTCTTCCCTGATCA
CCAGGTGCCTGTCTCCACAGGATCCCAGGGGATGGGGGTTAAGCTTGGCTCCTGGCGGTCCA
CCCTGCTGGAACCAGTTGAAACCCGTGTAATGGTGACCCTTTGAGCGAGCCAAGGCTGGGTG
GTAGATGACCATCTCTTGTCCAACAGGTCCCAGAGCAGTGGATATGTCTGGTCCTCCTAGTA
GCACAGAGGTGTGTTCTGGTGTGGTGGCAGGGACTTAGGGAATCCTACCACTCTGCTGGATT
TGGAACCCCCTAGGCTGACGCGGACGTATGCAGAGGCTCTCAAGGCCAGGCCCCACAGGGAG
GTGGAGGGGCTCCGGCCGCCACAGCCTGAATTCATGAACCTGGCAGGCACTTTGCCATAGCT
CATCTGAAAACAGATATTATGCTTCCCACAACCTCTCCTGGGCCCAGGTGTGGCTGAGCACC
AGGGATGGAGCCACACATAAGGGACAAATGAGTGCACGGTCCTACCTAGTCTTTCCTCACCT
CCTGAACTCACACAACAATGCCAGTCTCCCACTGGAGGCTGTATCCCCTCAGAGGAGCCAAG
GAATGTCTTCCCCTGAGATGCCACCACTATTAATTTCCCCATATGCTTCAACCACCCCCTTG
CTCAAAAAACCAATACCCACACTTACCTTAATACAAACATCCCAGCAACAGCACATGGCAGG
CCATTGCTGAGGGCACAGGTGCTTTATTGGAGAGGGGATGTGGGCAGGGGATAAGGAAGGTTCC
CCCATTCCAGGAGGATGGGAACAGTCCTGGCTGCCCCTGACAGTGGGGATATGCAAGGGGCT
CTGGCCAGGCCACAGTCCAAATGGGAAGACACCAGTCAGTCACAAAAGTCGGGAGCGCCACA
CAAACCTGGCTATAAGGCCCAGGAACCATATAGGAGCCTGAGACAGGTCCCCTGCACATTCA
TCATTAAACTATACAGGATGAGGCTGTACATGAGTTAATTACAAAAGAGTCATATTTACAAA
AATCTGTACACACATTTGAAAAACTCACAAAATTGTCATCTATGTATCACAAGTTGCTAGAC
CCAAAATATTAAAAATGGGATAAAATTNNTTTAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAA

# FIGURE 34

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA83505
><subunit 1 of 1, 402 aa, 1 stop
><MW: 43751, pI: 9.42, NX(S/T): 1
MRRRLRLRRDALLTLLLGASLGLLLYAQRDGAAPTASAPRGRGRAAPRPTPGPRAFQLPD
AGAAPPAYEGDTPAPPTPTGPFDFARYLRAKDQRRFPLLINQPHKCRGDGAPGGRPDLLI
AVKSVAEDFERRQAVRQTWGAEGRVQGALVRRVFLLGVPRGAGSGGADEVGEGARTHWRA
LLRAESLAYADILLWAFDDTFFNLTLKEIHFLAWASAFCPDVRFVFKGDADVFVNVGNLL
EFLAPRDPAQDLLAGDVIVHARPIRTRASKYYIPEAVYGLPAYPAYAGGGGFVLSGATLH
RLAGACAQVELFPIDDVFLGMCLQRLRLTPEPHPAFRTFGIPQPSAAPHLSTFDPCFYRE
LVVVHGLSAADIWLMWRLLHGPHGPACAHPQPVAAGPFQWDS

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-27

**N-glycosylation site:**
Amino acids 203-207

**N-myristoylation sites:**
Amino acids 18-24;31-37;110-116;157-163;161-167
163-169;366-372

**Cell attachment sequence:**
Amino acids 107-110

# FIGURE 35

AGCAGCCTCTGCCCGACCCGGCTCGTGCGGACCCCAGGACCGGGCGCGGGACGCGTGCGTCC
AGCCTCCGGCGCTGCGGAGACCCGCGGCTGGGTCCGGGGAGGCCCCAAACCCGCCCCCGCCA
GAACCCCGCCCCAAATTCCCACCTCCTCCAGAAGCCCCGCCCACTCCCGAGCCCCGAGAGCT
CCGCGCACCTGGGCGCCATCCGCCCTGGCTCCGCTGCACGAGCTCCACGCCCGTACCCCGGC
GTCACGCTCAGCCCGCGGTGCTCGCACACCTGAGACTCATCTCGCTTCGACCCCGCCGCCGC
CGCCGCCCGGCATCCTGAGCACGGAGACAGTCTCCAGCTGCCGTTC**ATG**CTTCCTCCCCAGC
CTTCCGCAGCCCACCAGGGAAGGGGCGGTAGGAGTGGCCTTTTACCAAAGGGACCGGCGATG
CTCTGCAGGCTGTGCTGGCTGGTCTCGTACAGCTTGGCTGTGCTGTTGCTCGGCTGCCTGCT
CTTCCTGAGGAAGGCGGCCAAGCCCGCAGGAGACCCCACGGCCCACCAGCCTTTCTGGGCTCCC
CCAACACCCCGTCACAGCCGGTGTCCACCCAACCACACAGTGTCTAGCGCCTCTCTGTCCCT
GCCTAGCCGTCACCGTCTCTTCTTGACCTATCGTCACTGCCGAAATTTCTCTATCTTGCTGG
AGCCTTCAGGCTGTTCCAAGGATACCTTCTTGCTCCTGGCCATCAAGTCACAGCCTGGTCAC
GTGGAGCGACGTGCGGCTATCCGCAGCACGTGGGGCAGGGTGGGGGGATGGGCTAGGGGCCG
GCAGCTGAAGCTGGTGTTCCTCCTAGGGGTGGCAGGATCCGCTCCCCCAGCCCAGCTGCTGG
CCTATGAGAGTAGGGAGTTTGATGACATCCTCCAGTGGGACTTCACTGAGGACTTCTTCAAC
CTGACGCTCAAGGAGCTGCACCTGCAGCGCTGGGTGGTGGCTGCCTGCCCCCAGGCCCATTT
CATGCTAAAGGGAGATGACGATGTCTTTGTCCACGTCCCCAACGTGTTAGAGTTCCTGGATG
GCTGGGACCCAGCCCAGGACCTCCTGGTGGGAGATGTCATCCGCCAAGCCCTGCCCAACAGG
AACACTAAGGTCAAATACTTCATCCCACCCTCAATGTACAGGGCCACCCACTACCCACCCTA
TGCTGGTGGGGGAGGATATGTCATGTCCAGAGCCACAGTGCGGCGCCTCCAGGCTATCATGG
AAGATGCTGAACTCTTCCCCATTGATGATGTCTTTGTGGGTATGTGCCTGAGGAGGCTGGGG
CTGAGCCCTATGCACCATGCTGGCTTCAAGACATTTGGAATCCGGCGGCCCCTGGACCCCTT
AGACCCCTGCCTGTATAGGGGGCTCCTGCTGGTTCACCGCCTCAGCCCCCTCGAGATGTGGA
CCATGTGGGCACTGGTGACAGATGAGGGGCTCAAGTGTGCAGCTGGCCCCATACCCCAGCGC
**TGA**AGGGTGGGTTGGGCAACAGCCTGAGAGTGGACTCAGTGTTGATTCTCTATCGTGATGCG
AAATTGATGCCTGCTGCTCTACAGAAAATGCCAACTTGGTTTTTTAACTCCTCTCACCCTGT
TAGCTCTGATTAAAAACACTGCAACCCAA

# FIGURE 36

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA84927
><subunit 1 of 1, 378 aa, 1 stop
><MW: 42310, pI: 9.58, NX(S/T): 3
MLPPQPSAAHQGRGGRSGLLPKGPAMLCRLCWLVSYSLAVLLLGCLLFLRKAAKPAGDPT
AHQPFWAPPTPRHSRCPPNHTVSSASLSLPSRHRLFLTYRHCRNFSILLEPSGCSKDTFL
LLAIKSQPGHVERRAAIRSTWGRVGGWARGRQLKLVFLLGVAGSAPPAQLLAYESREFDD
ILQWDFTEDFFNLTLKELHLQRWVVAACPQAHFMLKGDDDVFVHVPNVLEFLDGWDPAQD
LLVGDVIRQALPNRNTKVKYFIPPSMYRATHYPPYAGGGGYVMSRATVRRLQAIMEDAEL
FPIDDVFVGMCLRRLGLSPMHHAGFKTFGIRRPLDPLDPCLYRGLLLVHRLSPLEMWTMW
ALVTDEGLKCAAGPIPQR

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-39

**Transmembrane domain:**
Amino acids 146-171

**N-glycosylation sites:**
Amino acids 79-83;104-108;192-196

**N-myristoylation sites:**
Amino acids 14-20;160-166;367-373

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 35-46

# FIGURE 37

ATGAAAGTGATAATCAGGCAGCCCAAATGATTGTTAATAAGGATCAAATGAGATCGTGTATG
TGGGTCCAATCAATTGATTCTACACAAAGGAGCCTGGGGAGGGGCC**ATG**GTGCCAATGCACT
TACTGGGGAGACTGGAGAAGCCGCTTCTCCTCCTGTGCTGCGCCTCCTTCCTACTGGGGCTG
GCTTTGCTGGGCATAAAGACGGACATCACCCCCGTTGCTTATTTCTTTCTCACATTGGGTGG
CTTCTTCTTGTTTGCCTATCTCCTGGTCCGGTTTCTGGAATGGGGGCTTCGGTCCCAGCTCC
AATCAATGCAGACTGAGAGCCCAGGGCCCTCAGGCAATGCACGGGACAATGAAGCCTTTGAA
GTGCCAGTCTATGAAGAGGCCGTGGTGGGACTAGAATCCCAGTGCCGCCCCCAAGAGTTGGA
CCAACCACCCCCCTACAGCACTGTTGTGATACCCCCAGCACCTGAGGAGGAACAACCTAGCC
ATCCAGAGGGGTCCAGGAGAGCCAAACTGGAACAGAGGCGAATGGCCTCAGAGGGGTCCATG
GCCCAGGAAGGAAGCCCTGGAAGAGCTCCAATCAACCTTCGGCTTCGGGGACCACGGGCTGT
GTCCACTGCTCCTGATCTGCAGAGCTTGGCGGCAGTCCCCACATTAGAGCCTCTGACTCCAC
CCCCTGCCTATGATGTCTGCTTTGGTCACCCTGATGATGATAGTGTTTTTTATGAGGACAAC
TGGGCACCCCCT**TAA**ATGACTCTCCCAAGATTTCTCTTCTCTCCACACCAGACCTCGTTCAT
TTGACTAACATTTTCCAGCGCCTACTATGTGTCAGAAACAAGTGTTTCTGCCTGGACATCAT
AAATGGGGACTTGGACCCTGAGGAGAGTCAGGCCACGGTAAGCCCTTCCCAGCTGAGATATG
GGTGGCATAATTTGAGTCTTCTGGCAACATTTGGTGACCTACCCCATATCCAATATTTCCAG
CGTTAGATTGAGGATGAGGTAGGGAGGTGATCCAGAGAAGGCGGAGAAGGAAGAAGTAACCT
CTGAGTGGCGGCTATTGCTTCTGTTCCAGGTGCTGTTCGAGCTGTTAGAACCCTTAGGCTTGAC
AGCTTTGTGAGTTATTATTGAAAAATGAGGATTCCAAGAGTCAGAGGAGTTTGATAATGTGC
ACGAGGGCACACTGCTAGTAAATAACATTAAAATAACTGGAATGAA

# FIGURE 38

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA92264
><subunit 1 of 1, 216 aa, 1 stop
><MW: 23729, pI: 4.73, NX(S/T): 0
MVPMHLLGRLEKPLLLLCCASFLLGLALLGIKTDITPVAYFFLTLGGFFLFAYLLVRFLE
WGLRSQLQSMQTESPGPSGNARDNEAFEVPVYEEAVVGLESQCRPQELDQPPPYSTVVIP
PAPEEEQPSHPEGSRRAKLEQRRMASEGSMAQEGSPGRAPINLRLRGPRAVSTAPDLQSL
AAVPTLEPLTPPPAYDVCFGHPDDDSVFYEDNWAPP

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-25

**Transmembrane domain:**
Amino acids 41-59

**N-myristoylation site:**
Amino acids 133-139

# FIGURE 39

CCCACGCGTCCGGCGGCTACACACCTAGGTGCGGTGGGCTTCGGGTGGGGGGCCTGCAGCTA
GCTGATGGCAAGGGAGGAATAGCAGGGGTGGGGATTGTGGTGTGCGAGAGGTCCCGCGGACG
GGGGGCTCGGGGGTCTCTTCAGACGAGATTCCCTTCAGGCTTGGGCCGGGTCCCTTCGCACG
GAGATCCCAATGAACGCGGGCCCCTGGAGGCCGGTGGTTGGGGCTTCTCCGCGTCGGGGATG
GGGCCGGTACCCTAGCCCGTTTCCAGCGCCTCAGTCGGTTCCCC**ATG**CCCTCAGAGGTGGCC
CGGGGCAAGCGCGCCGCCCTCTTCTTCGCTGCGGTGGCCATCGTGCTGGGGCTACCGCTCTG
GTGGAAGACCACGGAGACCTACCGGGCCTCGTTGCCTTACTCCCAGATCAGTGGCCTGAATG
CCCTTCAGCTCCGCCTCATGGTGCCTGTCACTGTCGTGTTTACGCGGGAGTCAGTGCCCCTG
GACGACCAGGAGAAGCTGCCCTTCACCGTTGTGCATGAAAGAGAGATTCCTCTGAAATACAA
AATGAAAATCAAATGCCGTTTCCAGAAGGCCTATCGGAGGGCTTTGGACCATGAGGAGGAGG
CCCTGTCATCGGGCAGTGTGCAAGAGGCAGAAGCCATGTTAGATGAGCCTCAGGAACAAGCG
GAGGGCTCCCTGACTGTGTACGTGATATCTGAACACTCCTCACTTCTTCCCCAGGACATGAT
GAGCTACATTGGGCCCAAGAGGACAGCAGTGGTGCGGGGGATAATGCACCGGGAGGCCTTTA
ACATCATTGGCCGCCGCATAGTCCAGGTGGCCCAGGCCATGTCTTTGACTGAGGATGTGCTT
GCTGCTGCTCTGGCTGACCACCTTCCAGAGGACAAGTGGAGCGCTGAGAAGAGGCGGCCTCT
CAAGTCCAGCTTGGGCTATGAGATCACCTTCAGTTTACTCAACCCAGACCCCAAGTCCCATG
ATGTCTACTGGGACATTGAGGGGGCTGTCCGGCGCTATGTGCAACCTTTCCTGAATGCCCTC
GGTGCCGCTGGCAACTTCTCTGTGGACTCTCAGATTCTTTACTATGCAATGTTGGGGGTGAA
TCCCCGCTTTGACTCAGCTTCCTCCAGCTACTATTTGGACATGCACAGCCTCCCCCATGTCA
TCAACCCAGTGGAGTCCCGGCTGGGATCCAGTGCTGCCTCCTTGTACCCTGTGCTCAACTTT
CTACTCTACGTGCCTGAGCTTGCACACTCACCGCTGTACATTCAGGACAAGGATGGCGCTCC
AGTGGCCACCAATGCCTTCCATAGTCCCCGCTGGGGTGGCATTATGGTATATAATGTTGACT
CCAAAACCTATAATGCCTCAGTGCTGCCAGTGAGAGTCGAGGTGGACATGGTGCGAGTGATG
GAGGTGTTCCTGGCACAGTTGCGGTTGCTCTTTGGGATTGCTCAGCCCCAGCTGCCTCCAAA
ATGCCTGCTTTCAGGGCCTACGAGTGAAGGGCTAATGACCTGGGAGCTAGACCGGCTGCTCTGG
GCTCGGTCAGTGGAGAACCTGGCCACAGCCACCACCACCCTTACCTCCCTGGCGCAGCTTCT
GGGCAAGATCAGCAACATTGTCATTAAGGACGACGTGGCATCTGAGGTGTACAAGGCTGTAG
CTGCCGTCCAGAAGTCGGCAGAAGAGTTGGCGTCTGGGCACCTGGCATCTGCCTTTGTCGCC
AGCCAGGAAGCTGTGACATCCTCTGAGCTTGCCTTCTTTGACCCGTCACTCCTCCACCTCCT
TTATTTCCCTGATGACCAGAAGTTTGCCATCTACATCCCACTCTTCCTGCCTATGGCTGTGC
CCATCCTCCTGTCCCTGGTCAAGATCTTCCTGGAGACCCGCAAGTCCTGGAGAAAGCCTGAG
AAGACAGAC**TGA**GCAGGGCAGCACCTCCATAGGAAGCCTTCCTTTCTGGCCAAGGTGGGCGG
TGTTAGATTGTGAGGCACGTACATGGGGCCTGCCGGAATGACTTAAATATTTGTCTCCAGTC
TCCACTGTTGGCTCTCCAGCAACCAAAGTACAACACTCCAAGATGGGTTCATCTTTTCTTCC
TTTCCCATTCACCTGGCTCAATCCTCCTCCACCACCAGGGGCCTCAAAAGGCACATCATCCG
GGTCTCCTTATCTTGTTTGATAAGGCTGCTGCCTGTCTCCCTCTGTGGCAAGGACTGTTTGT
TCTTTTGCCCCATTTCTCAACATAGCACACTTGTGCACTGAGAGGAGGGAGCATTATGGGAA
AGTCCCTGCCTTCCACACCTCTCTCTAGTCCCTGTGGGACAGCCCTAGCCCCTGCTGTCATG
AAGGGGCCAGGCATTGGTCACCTGTGGGACCTTCTCCCTCACTCCCCTCCCTCCTAGTTGGC
TTTGTCTGTCAGGTGCAGTCTGGCGGGAGTCCAGGAGGCAGCAGCTCAGGACATGGTGCTGT
GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTCAGAGGTTCCAGAAAGTTCCAGATTT
GGAATCAAACAGTCCTGAATTCAAATCCTTGTTTTTGCACTTATTGTCTGGAGAGCTTTGGA
TAAGGTATTGAATCTCTCTGAGCCTCAGTTTTTCATTTGTTCAAATGGCACTGATGATGTCT
CCCTTACAAGATGGTTGTGAGGAGTAAATGTGATCAGCATGTAAAGTGTCTGGCGTGTAGTA
GGCTCTTAATAAACACTGGCTGAATATGAATTGGAATGAT

# FIGURE 40

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA94713
><subunit 1 of 1, 547 aa, 1 stop
><MW: 61005, pI: 6.34, NX(S/T): 2
MPSEVARGKRAALFFAAVAIVLGLPLWWKTTETYRASLPYSQISGLNALQLRLMVPVTVV
FTRESVPLDDQEKLPFTVVHEREIPLKYKMKIKCRFQKAYRRALDHEEEALSSGSVQEAE
AMLDEPQEQAEGSLTVYVISEHSSLLPQDMMSYIGPKRTAVVRGIMHREAFNIIGRRIVQ
VAQAMSLTEDVLAAALADHLPEDKWSAEKRRPLKSSLGYEITFSLLNPDPKSHDVYWDIE
GAVRRYVQPFLNALGAAGNFSVDSQILYYAMLGVNPRFDSASSSYYLDMHSLPHVINPVE
SRLGSSAASLYPVLNFLLYVPELAHSPLYIQDKDGAPVATNAFHSPRWGGIMVYNVDSKT
YNASVLPVRVEVDMVRVMEVFLAQLRLLFGIAQPQLPPKCLLSGPTSEGLMTWELDRLLW
ARSVENLATATTTLTSLAQLLGKISNIVIKDDVASEVYKAVAAVQKSAEELASGHLASAF
VASQEAVTSSELAFFDPSLLHLLYFPDDQKFAIYIPLFLPMAVPILLSLVKIFLETRKSW
RKPEKTD

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-23

**Transmembrane domain:**
Amino acids 511-530

**N-glycosylation sites:**
Amino acids 259-263;362-366

**N-myristoylation sites:**
Amino acids 255-261;304-310;335-341

**Amidation sites:**
Amino acids 7-11;174-178

# FIGURE 41

CCAGCTGCAGAGAGGAGGAGGTGAGCTGCAGAGAAGAGGAGGTTGGTGTGGAGCACAGGCAG
CACCGAGCCTGCCCCGTGAGCTGAGGGCCTGCAGTCTGCGGCTGGAATCAGGATAGACACCA
AGGCAGGACCCCCAGAGATGCTGAAGCCTCTTTGGAAAGCAGCAGTGGCCCCCACATGGCCA
TGCTCC**ATG**CCGCCCCGCCGCCCGTGGGACAGAGAGGCTGGCACGTTGCAGGTCCTGGGAGC
GCTGGCTGTGCTGTGGCTGGGCTCCGTGGCTCTTATCTGCCTCCTGTGGCAAGTGCCCCGTCCT
CCCACCTGGGGCCAGGTGCAGCCCAAGGACGTGCCCAGGTCCTGGGAGCATGGCTCCAGCCC
AGCTTGGGAGCCCCTGGAAGCAGAGGCCAGGCAGCAGAGGGACTCCTGCCAGCTTGTCCTTG
TGGAAAGCATCCCCCAGGACCTGCCATCTGCAGCCGGCAGCCCCTCTGCCCAGCCTCTGGGC
CAGGCCTGGCTGCAGCTGCTGGACACTGCCCAGGAGAGCGTCCACGTGGCTTCATACTACTG
GTCCCTCACAGGGCCTGACATCGGGGTCAACGACTCGTCTTCCCAGCTGGGAGAGGCTCTTC
TGCAGAAGCTGCAGCAGCTGCTGGGCAGGAACATTTCCCTGGCTGTGGCCACCAGCAGCCCG
ACACTGGCCAGGACATCCACCGACCTGCAGGTTCTGGCTGCCCGAGGTGCCCATGTACGACA
GGTGCCCATGGGGCGGCTCACCAGGGGTGTTTTGCACTCCAAATTCTGGGTTGTGGATGGAC
GGCACATATACATGGGCAGTGCCAACATGGACTGGCGGTCTCTGACGCAGGTGAAGGAGCTT
GGCGCTGTCATCTATAACTGCAGCCACCTGGCCCAAGACCTGGAGAAGACCTTCCAGACCTA
CTGGGTACTGGGGGTGCCCAAGGCTGTCCTCCCCAAAACCTGGCCTCAGAACTTCTCATCTC
ACTTCAACCGTTTCCAGCCCTTCCACGGCCTCTTTGATGGGGTGCCCACCACTGCCTACTTC
TCAGCGTCGCCACCAGCACTCTGTCCCCAGGGCCGCACCCGGGACCTGGAGGCGCTGCTGGC
GGTGATGGGGAGCGCCCAGGAGTTCATCTATGCCTCCGTGATGGAGTATTTCCCCACCACGC
GCTTCAGCCACCCCCCGAGGTACTGGCCGGTGCTGGACAACGCGCTGCGGGCGGCAGCCTTC
GGCAAGGGCGTGCGCGTGCGCCTGCTGGTCGGCTGCGGACTCAACACGGACCCCACCATGTT
CCCCTACCTGCGGTCCCTGCAGGCGCTCAGCAACCCCGCGGCCAACGTCTCTGTGGACGTGA
AAGTCTTCATCGTGCCGGTGGGGAACCATTCCAACATCCCATTCAGCAGGGTGAACCACAGC
AAGTTCATGGTCACGGAGAAGGCAGCCTACATAGGCACCTCCAACTGGTCGGAGGATTACTT
CAGCAGCACGGCGGGGGTGGGCTTGGTGGTCACCCAGAGCCCTGGCGCGCAGCCCGCGGGGG
CCACGGTGCAGGAGCAGCTGCGGCAGCTCTTTGAGCGGGACTGGAGTTCGCGCTACGCCGTC
GGCCTGGACGGACAGGCTCCGGGCCAGGACTGCGTTTGGCAGGGC**TGA**GGGGGGCCTCTTTT
TCTCTCGGCGACCCCGCCCCGCACGCGCCCTCCCCTCTGACCCCGGCCTGGGCTTCAGCCGC
TTCCTCCCGCAAGCAGCCCGGGTCCGCACTGCGCCAGGAGCCGCCTGCGACCGCCCGGGCGT
CGCAAACCGCCCGCCTGCTCTCTGATTTCCGAGTCCAGCCCCCCCTGAGCCCCACCTCCTCC
AGGGAGCCCTCCAGGAAGCCCCTTCCCTGACTCCTGGCCCACAGGCCAGGCCTAAAAAAAAC
TCGTGGCTTCAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 42

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96869
><subunit 1 of 1, 489 aa, 1 stop
><MW: 53745, pI: 8.36, NX(S/T): 8
MPPRRPWDREAGTLQVLGALAVLWLGSVALICLLWQVPRPPTWGQVQPKDVPRSWEHGSS
PAWEPLEAEARQQRDSCQLVLVESIPQDLPSAAGSPSAQPLGQAWLQLLDTAQESVHVAS
YYWSLTGPDIGVNDSSSQLGEALLQKLQQLLGRNISLAVATSSPTLARTSTDLQVLAARG
AHVRQVPMGRLTRGVLHSKFWVVDGRHIYMGSANMDWRSLTQVKELGAVIYNCSHLAQDL
EKTFQTYWVLGVPKAVLPKTWPQNFSSHFNRFQPFHGLFDGVPTTAYFSASPPALCPQGR
TRDLEALLAVMGSAQEFIYASVMEYFPTTRFSHPPRYWPVLDNALRAAAFGKGVRVRLLV
GCGLNTDPTMFPYLRSLQALSNPAANVSVDVKVFIVPVGNHSNIPFSRVNHSKFMVTEKA
AYIGTSNWSEDYFSSTAGVGLVVTQSPGAQPAGATVQEQLRQLFERDWSSRYAVGLDGQA
PGQDCVWQG

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-29

**N-glycosylation sites:**
Amino acids 133-137;154-158;232-236;264-268;
386-390;400-404;410-414;427-431

**N-myristoylation sites:**
Amino acids 58-64;94-100;131-137;194-200;251-257;
277-283;281-287;361-367;399-405;
440-446;448-454;478-484

# FIGURE 43

GGGCCTGGCGATCCGGATCCCGCAGGCGCGCTGGCTGCGCTGCCCGGCTGTCTGTCGTC**ATG**
GTGGGGCCCTGGGTGTATCTGGTGGCGGCAGTTTTGCTCATCGGCCTGATCCTCTTCCTGAC
TCGCAGCCGGGGTCGGGCGGCAGCAGCTGACGGAGAACCACTGCACAATGAGGAAGAGAGGG
CAGGAGCAGGCCAGGTAGGCCGCTCTTTGCCCCAGGAGTCTGAAGAACAGAGAACTGGAAGC
AGACCCCGGCGTCGGAGGGACTTGGGCAGCCGTCTACAGGCCCAGCGTCGAGCCCAGCGAGT
GGCCTGGGAAGACGGGGATGAGAATGTGGGTCAAACTGTTATTCCAGCCCAGGAGGAAGAAG
GCATTGAGAAGCCAGCAGAAGTTCACCCAACAGGGAAAATTGGAGCCAAGAAACTACGGAAG
CTAGAGGAAAAACAGGCTCGAAAGGCTCAGCGAGAGGCAGAGGAGGCTGAACGTGAAGAACG
GAAACGCCTAGAGTCCCAACGTGAGGCCGAATGGAAGAAGGAAGAGGAACGGCTTCGCCTGA
AGGAAGAACAGAAGGAGGAGGAAGAGAGGAAGGCTCAGGAGGAGCAGGCCCGGCGGGATCAC
GAGGAGTACCTGAAACTGAAGGAGGCCTTCGTGGTAGAAGAAGAAGGTGTTAGCGAAACCAT
GACTGAGGAGCAGTCTCACAGCTTCCTGACAGAATTCATCAATTACATCAAGAAGTCCAAGG
TTGTGCTTTTGGAAGATCTGGCTTTCCAGATGGGCCTAAGGACTCAGGACGCCATAAACCGC
ATCCAGGACCTGCTGACGGAGGGGACTCTAACAGGTGTGATTGACGACCGGGGCAAGTTTAT
CTACATAACCCCAGAGGAACTGGCTGCCGTGGCCAATTTCATCCGACAGCGGGGCCGGGTGT
CCATCACAGAGCTTGCCCAGGCCAGCAACTCCCTCATCTCCTGGGGCCAGGACCTCCCTGCC
CAGGCTTCAGCC**TGA**CTCCAGTCCTTCCTTGAGTGTATCCTGTGGCCTACATGTGTCTTCAT
CCTTCCCTAATGCCGTCTTGGGGCAGGGATGGAATATGACCAGAAAGTTGTGGATTAAAGGC
CTGTGAATACTGAA

# FIGURE 44

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96881
><subunit 1 of 1, 315 aa, 1 stop
><MW: 35963, pI: 5.38, NX(S/T): 0
MVGPWVYLVAAVLLIGLILFLTRSRGRAAAADGEPLHNEEERAGAGQVGRSLPQESEEQR
TGSRPRRRRDLGSRLQAQRRAQRVAWEDGDENVGQTVIPAQEEEGIEKPAEVHPTGKIGA
KKLRKLEEKQARKAQREAEEAEREERKRLESQREAEWKKEEERLRLKEEQKEEEERKAQE
EQARRDHEEYLKLKEAFVVEEEGVSETMTEEQSHSFLTEFINYIKKSKVVLLEDLAFQMG
LRTQDAINRIQDLLTEGTLTGVIDDRGKFIYITPEELAAVANFIRQRGRVSITELAQASN
SLISWGQDLPAQASA

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-26

**N-myristoylation sites:**
Amino acids 203-209;257-263

# FIGURE 45

ACGGGCCGCAGCGGCAGTGACGTAGGGTTGGCGCACGGATCCGTTGCGGCTGCAGCTCTGCA
GTCGGGCCGTTCCTTCGCCGCCGCCAGGGGTAGCGGTGTAGCTGCGCAGCGTCGCGCGCGCT
ACCGCACCCAGGTTCGGCCCGTAGGCGTCTGGCAGCCCGGCGCCATCTTCATCGAGCGCC**AT**
**G**GCCGCAGCCTGCGGGCCGGGAGCGGCCGGGTACTGCTTGCTCCTCGGCTTGCATTTGTTTC
TGCTGACCGCGGGCCCTGCCCTGGGCTGGAACGACCCTGACAGAATGTTGCTGCGGGATGTA
AAAGCTCTTACCCTCCACTATGACCGCTATACCACCTCCCGCAGGCTGGATCCCATCCCACA
GTTGAAATGTGTTGGAGGCACAGCTGGTTGTGATTCTTATACCCCAAAAGTCATACAGTGTC
AGAACAAAGGCTGGGATGGGTATGATGTACAGTGGGAATGTAAGACGGACTTAGATATTGCA
TACAAATTTGGAAAAACTGTGGTGAGCTGTGAAGGCTATGAGTCCTCTGAAGACCAGTATGT
ACTAAGAGGTTCTTGTGGCTTGGAGTATAATTTAGATTATACAGAACTTGGCCTGCAGAAAC
TGAAGGAGTCTGGAAAGCAGCACGGCTTTGCCTCTTTCTCTGATTATTATTATAAGTGGTCC
TCGGCGGATTCCTGTAACATGAGTGGATTGATTACCATCGTGGTACTCCTTGGGATCGCCTT
TGTAGTCTATAAGCTGTTCCTGAGTGACGGGCAGTATTCTCCTCCACCGTACTCTGAGTATC
CTCCATTTTCCCACCGTTACCAGAGATTCACCAACTCAGCAGGACCTCCTCCCCCAGGCTTT
AAGTCTGAGTTCACAGGACCACAGAATACTGGCCATGGTGCAACTTCTGGTTTTGGCAGTGC
TTTTACAGGACAACAAGGATATGAAAATTCAGGACCAGGGTTCTGGACAGGCTTGGGAACTG
GTGGAATACTAGGATATTTGTTTGGCAGCAATAGAGCGGCAACACCCTTCTCAGACTCGTGG
TACTACCCGTCCTATCCTCCCTCCTACCCTGGCACGTGGAATAGGGCTTACTCACCCCTTCA
TGGAGGCTCGGGCAGCTATTCGGTATGTTCAAACTCAGACACGAAAACCAGAACTGCATCAG
GATATGGTGGTACCAGGAGACGA**TAA**AGTAGAAAGTTGGAGTCAAACACTGGATGCAGAAAT
TTTGGATTTTTCATCACTTTCTCTTTAGAAAAAAAGTACTACCTGTTAACAATTGGGAAAAG
GGGATATTCAAAAGTTCTGTGGTGTTATGTCCAGTGTAGCTTTTTGTATTCTATTATTTGAG
GCTAAAAGTTGATGTGTGACAAAATACTTATGTGTTGTATGTCAGTGTAACATGCAGATGTA
TATTGCAGTTTTTGAAAGTGATCATTACTGTGGAATGCTAAAAATACATTAATTTCTAAAAC
CTGTGATGCCCTAAGAAGCATTAAGAATGAAGGTGTTGTACTAATAGAAACTAAGTACAGAA
AATTTCAGTTTTAGGTGGTTGTAGCTGATGAGTTATTACCTCATAGAGACTATAATATTCTA
TTTGGTATTATATTATTTGATGTTTGCTGTTCTTCAAACATTTAAATCAAGCTTTGGACTAA
TTATGCTAATTTGTGAGTTCTGATCACTTTTGAGCTCTGAAGCTTTGAATCATTCAGTGGTG
GAGATGGCCTTCTGGTAACTGAATATTACCTTCTGTAGGAAAAGGTGGAAAATAAGCATCTA
GAAGGTTGTTGTGAATGACTCTGTGCTGGCAAAAATGCTTGAAACCTCTATATTTCTTTCGT
TCATAAGAGGTAAAGGTCAAATTTTTCAACAAAAGTCTTTTAATAACAAAAGCATGCAGTTCTC
TGTGAAATCTCAAATATTGTTGTAATAGTCTGTTTCAATCTTAAAAAGAATCA

# FIGURE 46

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96889
><subunit 1 of 1, 339 aa, 1 stop
><MW: 36975, pI: 7.85, NX(S/T): 1
MAAACGPGAAGYCLLLGLHLFLLTAGPALGWNDPDRMLLRDVKALTLHYDRYTTSRRLDP
IPQLKCVGGTAGCDSYTPKVIQCQNKGWDGYDVQWECKTDLDIAYKFGKTVVSCEGYESS
EDQYVLRGSCGLEYNLDYTELGLQKLKESGKQHGFASFSDYYYKWSSADSCNMSGLITIV
VLLGIAFVVYKLFLSDGQYSPPPYSEYPPFSHRYQRFTNSAGPPPPGFKSEFTGPQNTGH
GATSGFGSAFTGQQGYENSGPGFWTGLGTGGILGYLFGSNRAATPFSDSWYYPSYPPSYP
GTWNRAYSPLHGGSGSYSVCSNSDTKTRTASGYGGTRRR

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-30

**Transmembrane domain:**
Amino acids 171-190

**N-glycosylation site:**
Amino acids 172-176

**Glycosaminoglycan attachment sites:**
Amino acids 244-248;259-263;331-335

**Tyrosine kinase phosphorylation site:**
Amino acids 98-106

**N-myristoylation sites:**
Amino acids 68-74;69-75;131-137;241-247;
247-253;266-272;270-276;278-284;
312-318

# FIGURE 47

CCCGGAGCCGGGGAGGGAGGGAGCGAGGTTCGGACACCGGCGGCGGCTGCCTGGCCTTTCCA
TGAGCCCGCGGCGGACCCTCCCGCGCCCCCTCTCGCTCTGCCTCTCCCTCTGCCTCTGCCTC
TGCCTGGCCGCGGCTCTGGGAAGTGCGCAGTCCGGGTCGTGTAGGGATAAAAAGAACTGTAA
GGTGGTCTTTTCCCAGCAGGAACTGAGGAAGCGGCTAACACCCCTGCAGTACCATGTCACTC
AGGAGAAAGGGACCGAAAGTGCCTTTGAAGGAGAATACACACATCACAAAGATCCTGGAATA
TATAAATGTGTTGTTTGTGGAACTCCATTGTTTAAGTCAGAAACCAAATTTGACTCCGGTTC
AGGTTGGCCTTCATTCCACGATGTGATCAATTCTGAGGCAATCACATTCACAGATGACTTTT
CCTATGGGATGCACAGGGTGGAAACAAGCTGCTCTCAGTGTGGTGCTCACCTTGGGCACATT
TTTGATGATGGGCCTCGTCCAACTGGGAAAAGATACTGCATAAATTCGGCTGCCTTGTCTTT
TACACCTGCGGATAGCAGTGGCACCGCCGAGGGAGGCAGTGGGGTCGCCAGCCCGGCCCAGG
CAGACAAAGCGGAGCTCTAGAGTAATGGAGAGTGATGGAAACAAAGTGTACTTAATGCACAG
CTTATTAAAAAAATCAAAATTGTTATCTTAATAGATATATTTTTTCAAAAACTATAAGGGCA
GTTTTGTGCTATTGATATTTTTTCTTCTTTTGCTTAAACAGAAGCCCTGGCCATCCATGTAT
TTTGCAATTGACTAGATCAAGAACTGTTTATAGCTTTAGCAAATGGAGACAGCTTTGTGAAA
CTTCTTCACAAGCCACTTATACCCTTTGGCATTCTTTTCTTTGAGCACATGGCTTCTTTTGC
AGTTTTTCCCCCTTTGATTCAGAAGCAGAGGGTTCATGGTCTTCAAACATGAAAATAGAGAT
CTCCTCTGCAGTGTAGAGACCAGAGCTGGGCAGTGCAGGGCATGGAGACCTGCAAGACACAT
GGCCTTGAGGCCTTTGCACAGACCCACCTAAGATAAGGTTGGAGTGATGTTTTAATGAGACT
GTTCAGCTTTGTGGAAAGTTTGAGCTAAGGTCATTTTTTTTTTTCTCACTGAAAGGGTGTGA
AGGTCTAAAGTCTTTCCTTATGTTAAATTGTTGCCAGATCCAAAGGGGCATACTGAGTGTTG
TGGCAGAGAAGTAAACATTACCACACTGTTAGGCCTTTATTTTATTTTATTTTCCATCGAAA
GCATTGGAGGCCCAGTGCAATGGCTCACGCCTGTGATCCCAGCACTTTGGGAGGCCAAGGCG
GGTGGATCACGAGGTCAGGAGATGGAGACCATCCTGGCTAACATGGTGAAACCCCGTCTCTA
CTAAAAATACGAAAAATTAGCCAGGCGTGGTGGTGGGCACCTGTAGTCCCAGCTACTCAGGAGG
CTGAGGCAGGAGAATGGCGTGAACCCGGAAGGCGGAGCTTGCAGTTAGCCGAGATCATGCCA
CTGCACTCCAGCCTACATGACAATGTGACACTCCATCTCAAAAAATAATAATAATAACAATA
TAAGAACTAGCTGGGCATGGTGGCGCATGCATGTAGTCCCAGCTACTCCTGAGGCTCAGTCA
GGAGAATCGCTTGAACTTGGGAGGCGGAGGTTGCAGTGAGCTGAGCTCATACCACTGCACTC
CAGCCTGAACAGAGTGAGATCCTGTCAA

# FIGURE 48

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96898
><subunit 1 of 1, 192 aa, 1 stop
><MW: 20702, pI: 7.50, NX(S/T): 0
MSPRRTLPRPLSLCLSLCLCLCLAAALGSAQSGSCRDKKNCKVVFSQQELRKRLTPLQYH
VTQEKGTESAFEGEYTHHKDPGIYKCVVCGTPLFKSETKFDSGSGWPSFHDVINSEAITF
TDDFSYGMHRVETSCSQCGAHLGHIFDDGPRPTGKRYCINSAALSFTPADSSGTAEGGSG
VASPAQADKAEL

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-24

**Glycosaminoglycan attachment site:**
Amino acids 102-106

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 52-56

**N-myristoylation sites:**
Amino acids 28-34;66-72;82-88;139-145;
173-179;178-184

**Amidation site:**
Amino acids 153-157

# FIGURE 49

CCCAAAGAGGTGAGGAGCCGGCAGCGGGGGCGGCTGTAACTGTGAGGAAGGCTGCAGAGTGG
CGACGTCTACGCCGTAGGTTGGAGGCTGTGGGGGGTGGCCGGGCGCCAGCTCCCAGGCCGCA
GAAGTGACCTGCGGTGGAGTTCCCTCCTCGCTGCTGGAGAACGGAGGGAGAAGGTTGCTGGC
CGGGTGAAAGTGCCTCCCTCTGCTTGACGGGGCTGAGGGGCCCGAAGTCTAGGGCGTCCGTA
GTCGCCCCGGCCTCCGTGAAGCCCCAGGTCTAGAGAT**ATG**ACCCGAGAGTGCCCATCTCCGG
CCCCGGGGCCTGGGGCTCCGCTGAGTGGATCGGTGCTGGCAGAGGCGGCAGTAGTGTTTGCA
GTGGTGCTGAGCATCCACGCAACCGTATGGGACCGATACTCGTGGTGCGCCGTGGCCCTCGC
AGTGCAGGCCTTCTACGTCCAATACAAGTGGGACCGGCTGCTACAGCAGGGAAGCGCCGTCT
TCCAGTTCCGAATGTCCGCAAACAGTGGCCTATTGCCCGCCTCCATGGTCATGCCTTTGCTT
GGACTAGTCATGAAGGAGCGGTGCCAGACTGCTGGGAACCCGTTCTTTGAGCGTTTTGGCAT
TGTGGTGGCAGCCACTGGCATGGCAGTGGCCCTCTTCTCATCAGTGTTGGCGCTCGGCATCA
CTCGCCCAGTGCCAACCAACACTTGTGTCATCTTGGGCTTGGCTGGAGGTGTTATCATTTAT
ATCATGAAGCACTCGTTGAGCGTGGGGGAGGTGATCGAAGTCCTGGAAGTCCTTCTGATCTT
CGTTTATCTCAACATGATCCTGCTGTACCTGCTGCCCCGCTGCTTCACCCCTGGTGAGGCAC
TGCTGGTATTGGGTGGCATTAGCTTTGTCCTCAACCAGCTCATCAAGCGCTCTCTGACACTG
GTGGAAAGTCAGGGGGACCCAGTGGACTTCTTCCTGCTGGTGGTGGTAGTAGGGATGGTACT
CATGGGCATTTTCTTCAGCACTCTGTTTGTCTTCATGGACTCAGGCACCTGGGCCTCCTCCA
TCTTCTTCCACCTCATGACCTGTGTGCTGAGCCTTGGTGTGGTCCTACCCTGGCTGCACCGG
CTCATCCGCAGGAATCCCCTGCTCTGGCTTCTTCAGTTTCTCTTCCAGACAGACACCCGCAT
CTACCTCCTAGCCTATTGGTCTCTGCTGGCCACCTTGGCCTGCCTGGTGGTGCTGTACCAGA
ATGCCAAGCGGTCATCTTCCGAGTCCAAGAAGCACCAGGCCCCCACCATCGCCCGAAAGTAT
TTCCACCTCATTGTGGTAGCCACCTACATCCCAGGTATCATCTTTGACCGGCCACTGCTCTAT
GTAGCCGCCACTGTATGCCTGGCGGTCTTCATCTTCCTGGAGTATGTGCGCTACTTCCGCAT
CAAGCCTTTGGGTCACACTCTACGGAGCTTCCTGTCCCTTTTTCTGGATGAACGAGACAGTG
GACCACTCATTCTGACACACATCTACCTGCTCCTGGGCATGTCTCTTCCCATCTGGCTGATC
CCCAGACCCTGCACACAGAAGGGTAGCCTGGGAGGAGCCAGGGCCCTCGTCCCCTATGCCGG
TGTCCTGGCTGTGGGTGTGGGTGATACTGTGGCCTCCATCTTCGGTAGCACCATGGGGGAGA
TCCGCTGGCCTGGAACCAAAAAGACTTTTGAGGGGACCATGACATCTATATTTGCGCAGATC
ATTTCTGTAGCTCTGATCTTAATCTTTGACAGTGGAGTGGACCTAAACTACAGTTATGCTTG
GATTTTGGGGTCCATCAGCACTGTGTCCCTCCTGGAAGCATACACTACACAGATAGACAATC
TCCTTCTGCCTCTCTACCTCCTGATATTGCTGATGGCC**TAG**CTGTTACAGTGCAGCAGCAGT
GACGGAGGAAACAGACATGGGGAGGGTGAACAGTCCCCACAGCAGACAGCTACTTGGGCATG
AAGAGCCAAGGTGTGAAAAGCAGATTTGATTTTTCAGTTGATTCAGATTTAAAATAAAAAGC
AAAGCTCTCCTAGTTCTA

# FIGURE 50

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA97003
><subunit 1 of 1, 538 aa, 1 stop
><MW: 59268, pI: 8.94, NX(S/T): 1
MTRECPSPAPGPGAPLSGSVLAEAAVVFAVVLSIHATVWDRYSWCAVALAVQAFYVQYKW
DRLLQQGSAVFQFRMSANSGLLPASMVMPLLGLVMKERCQTAGNPFFERFGIVVAATGMA
VALFSSVLALGITRPVPTNTCVILGLAGGVIIYIMKHSLSVGEVIEVLEVLLIFVYLNMI
LLYLLPRCFTPGEALLVLGGISFVLNQLIKRSLTLVESQGDPVDFFLLVVVVGMVLMGIF
FSTLFVFMDSGTWASSIFFHLMTCVLSLGVVLPWLHRLIRRNPLLWLLQFLFQTDTRIYL
LAYWSLLATLACLVVLYQNAKRSSSESKKHQAPTIARKYFHLIVVATYIPGIIFDRPLLY
VAATVCLAVFIFLEYVRYFRIKPLGHTLRSFLSLFLDERDSGPLILTHIYLLLGMSLPIW
LIPRPCTQKGSLGGARALVPYAGVLAVGVGDTVASIFGSTMGEIRWPGTKKTFEGTMTSI
FAQIISVALILIFDSGVDLNYSYAWILGSISTVSLLEAYTTQIDNLLLPLYLLILLMA

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-36

**Transmembrane domains:**
Amino acids 77-95;111-133;161-184;225-248;
255-273;299-314;348-373;406-421;
435-456;480-497

**N-glycosylation sites:**
Amino acids 500-504

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 321-325

**N-myristoylation sites:**
Amino acids 13-19;18-24;80-86;111-117;
118-124;145-151;238-244;251-257;
430-436;433-439;448-454;458-464;
468-474;475-481;496-502;508-514

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 302-313

# FIGURE 51

GCTCTATGCCGCCTACCTTGCTCTCGCCGCTGCTGCCGGAGCCGAAGCAGAGAAGGCAGCGGGTCCCGTGACCG
TCCCGAGAGCCCCGCGCTCCCGACCAGGGGGCGGGGGCGGCCCCGGGGAGGGCGGGGCAGGGGCGGGGGGAAGA
AAGGGGGTTTTGTGCTGCGCCGGGAGGGCCGGCGCCCTCTTCCGAATGTCCTGCGGCCCCAGCCTCTCCTCACG
CTCGCGCAGTCTCCGCCGCAGTCTCAGCTGCAGCTGCAGGACTGAGCCGTGCACCCGGAGGAGACCCCCGGAGG
AGGCGACAAACTTCGCAGTGCCGCGACCCAACCCCAGCCCTGGGTAGCCTGCAGCATGGCCCAGCTGTTCCTGC
CCCTGCTGGCAGCCCTGGTCCTGGCCCAGGCTCCTGCAGCTTTAGCAGATGTTCTGGAAGGAGACAGCTCAGAG
GACCGCGCTTTTCGCGTGCGCATCGCGGGCGACGCGCCACTGCAGGGCGTGCTCGGCGGCGCCCTCACCATCCC
TTGCCACGTCCACTACCTGCGGCCACCGCCGAGCCGCCGGGCTGTGCTGGGCTCTCCGCGGGTCAAGTGGACTT
TCCTGTCCCGGGGCCGGGAGGCAGAGGTGCTGGTGGCGCGGGGAGTGCGCGTCAAGGTGAACGAGGCCTACCGG
TTCCGCGTGGCACTGCCTGCGTACCCAGCGTCGCTCACCGACGTCTCCCTGGCGCTGAGCGAGCTGCGCCCCAA
CGACTCAGGTATCTATCGCTGTGAGGTCCAGCACGGCATCGATGACAGCAGCGACGCTGTGGAGGTCAAGGTCA
AAGGGGTCGTCTTTCTCTACCGAGAGGGCTCTGCCCGCTATGCTTTCTCCTTTTCTGGGGCCCAGGAGGCCTGT
GCCCGCATTGGAGCCCACATCGCCACCCCGGAGCAGCTCTATGCCGCCTACCTTGGGGGCTATGAGCAATGTGA
TGCTGGCTGGCTGTCGGATCAGACCGTGAGGTATCCCATCCAGACCCCACGAGAGGCCTGTTACGGAGACATGG
ATGGCTTCCCCGGGGTCCGGAACTATGGTGTGGTGGACCCGGATGACCTCTATGATGTGTACTGTTATGCTGAA
GACCTAAATGGAGAACTGTTCCTGGGTGACCCTCCAGAGAAGCTGACATTGGAGGAAGCACGGGCGTACTGCCA
GGAGCGGGGTGCAGAGATTGCCACCACGGGCCAACTGTATGCAGCCTGGGATGGTGGCCTGGACCACTGCAGCC
CAGGGTGGCTAGCTGATGGCAGTGTGCGCTACCCCATCGTCACACCCAGCCAGCGCTGTGGTGGGGGCTTGCCT
GGTGTCAAGACTCTCTTCCTCTTCCCCAACCAGACTGGCTTCCCCAATAAGCACAGCCGCTTCAACGTCTACTG
CTTCCGAGACTCGGCCCAGCCTTCTGCCATCCCTGAGGCCTCCAACCCAGCCTCCAACCCAGCCTCTGATGGAC
TAGAGGCTATCGTCACAGTGACAGAGACCCTGGAGGAACTGCAGCTGCCTCAGGAAGCCACAGAGAGTGAATCC
CGTGGGGCCATCTACTCCATCCCCATCATGGAGGACGGAGGAGGTGGAAGCTCCACTCCAGAAGACCCAGCAGA
GGCCCCTAGGACGCTCCTAGAATTTGAAACACAATCCATGGTACCGCCCACGGGGTTCTCAGAAGAGGAAGGTA
AGGCATTGGAGGAAGAAGAGAAATATGAAGATGAAGAAGAGAAAGAGGAGGAAGAAGAAGAGGAGGAGGTGGAG
GATGAGGCTCTGTGGGCATGGCCCAGCGAGCTCAGCAGCCCGGGCCCTGAGGCCTCTCTCCCCACTGAGCCAGC
AGCCCAGGAGAAGTCACTCTCCCAGGCGCCAGCAAGGGCAGTCCTGCAGCCTGGTGCATCACCACTTCCTGATG
GAGAGTCAGAAGCTTCCAGGCCTCCAAGGGTCCATGGACCACCTACTGAGACTCTGCCCACTCCCAGGGAGAGG
AACCTAGCATCCCCATCACCTTCCACTCTGGTTGAGGCAAGAGAGGTGGGGGAGGCAACTGGTGGTCCTGAGCT
ATCTGGGGTCCCTCGAGGAGAGAGCGAGGAGACAGGAAGCTCCGAGGGTGCCCCTTCCCTGCTTCCAGCCACAC
GGGCCCCTGAGGGTACCAGGGAGCTGGAGGCCCCCTCTGAAGATAATTCTGGAAGAACTGCCCCAGCAGGGACC
TCAGTGCAGGCCCAGCCAGTGCTGCCCACTGACAGCGCCAGCCGAGGTGGAGTGGCCGTGGTCCCCGCATCAGG
TGACTGTGTCCCCAGCCCCTGCCACAATGGTGGGACATGCTTGGAGGAGGAGGAAGGGGTCCGCTGCCTATGTC
TGCCTGGCTATGGGGGGGACCTGTGCGATGTTGGCCTCCGCTTCTGCAACCCCGGCTGGGACGCCTTCCAGGGC
GCCTGCTACAAGCACTTTTCCACACGAAGGAGCTGGGAGGAGGCAGAGACCCAGTGCCGGATGTACGGCGCGCA
TCTGGCCAGCATCAGCACACCCGAGGAACAGGACTTCATCAACAACCGGTACCGGGAGTACCAGTGGATCGGAC
TCAACGACAGGACCATCGAAGGCGACTTCTTGTGGTCGGATGGCGTCCCCCTGCTCTATGAGAACTGGAACCCT
GGGCAGCCTGACAGCTACTTCCTGTCTGGAGAGAACTGCGTGGTCATGGTGTGGCATGATCAGGGACAATGGAG
TGACGTGCCCTGCAACTACCACCTGTCCTACACCTGCAAGATGGGGCTGGTGTCCTGTGGGCCGCCACCGGAGC
TGCCCCTGGCTCAAGTGTTCGGCCGCCCACGGCTGCGCTATGAGGTGGACACTGTGCTTCGCTACCGGTGCCGG
GAAGGACTGGCCCAGCGCAATCTGCCGCTGATCCGATGCCAAGAGAACGGTCGTTGGGAGGCCCCCCAGATCTC
CTGTGTGCCCAGAAGACCTGCCCGAGCTCTGCACCCAGAGGAGGACCCAGAAGGACGTCAGGGGAGGCTACTGG
GACGCTGGAAGGCGCTGTTGATCCCCCCTTCCAGCCCCATGCCAGGTCCCTAGGGGGCAAGGCCTTGAACACTGCCG
GCCACAGCACTGCCCTGTCACCCAAATTTTCCCTCACACCTTGCGCTCCCGCCACCACAGGAAGTGACAACATG
ACGAGGGGTGGTGCTGGAGTCCAGGTGACAGTTCCTGAAGGGGCTTCTGGGAAATACCTAGGAGGCTCCAGCCC
AGCCCAGGCCCTCTCCCCCTACCCTGGGCACCAGATCTTCCATCAGGGCCGGAGTAAATCCCTAAGTGCCTCAA
CTGCCCTCTCCCTGGCAGCCATCTTGTCCCCTCTATTCCTCTAGGGAGCACTGTGCCCACTCTTTCTGGGTTTT
CCAAGGGAATGGGCTTGCAGGATGGAGTGTCTGTAAAATCAACAGGAAATAAAACTGTGTATGAGCCCA

# FIGURE 52

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA98565
><subunit 1 of 1, 911 aa, 1 stop
><MW: 99117, pI: 4.62, NX(S/T): 2
MAQLFLPLLAALVLAQAPAALADVLEGDSSEDRAFRVRIAGDAPLQGVLGGALTIPCHVH
YLRPPPSRRAVLGSPRVKWTFLSRGREAEVLVARGVRVKVNEAYRFRVALPAYPASLTDV
SLALSELRPNDSGIYRCEVQHGIDDSSDAVEVKVKGVVFLYREGSARYAFSFSGAQEACA
RIGAHIATPEQLYAAYLGGYEQCDAGWLSDQTVRYPIQTPREACYGDMDGFPGVRNYGVV
DPDDLYDVYCYAEDLNGELFLGDPPEKLTLEEARAYCQERGAEIATTGQLYAAWDGGLDH
CSPGWLADGSVRYPIVTPSQRCGGGLPGVKTLFLFPNQTGFPNKHSRFNVYCFRDSAQPS
AIPEASNPASNPASDGLEAIVTVTETLEELQLPQEATESESRGAIYSIPIMEDGGGGSST
PEDPAEAPRTLLEFETQSMVPPTGFSEEEGKALEEEEKYEDEEEKEEEEEEEEVEDEALW
AWPSELSSPGPEASLPTEPAAQEKSLSQAPARAVLQPGASPLPDGESEASRPPRVHGPPT
ETLPTPRERNLASPSPSTLVEAREVGEATGGPELSGVPRGESEETGSSEGAPSLLPATRA
PEGTRELEAPSEDNSGRTAPAGTSVQAQPVLPTDSASRGGVAVVPASGDCVPSPCHNGGT
CLEEEEGVRCLCLPGYGGDLCDVGLRFCNPGWDAFQGACYKHFSTRRSWEEAETQCRMYG
AHLASISTPEEQDFINNRYREYQWIGLNDRTIEGDFLWSDGVPLLYENWNPGQPDSYFLS
GENCVVMVWHDQGQWSDVPCNYHLSYTCKMGLVSCGPPPELPLAQVFGRPRLRYEVDTVL
RYRCREGLAQRNLPLIRCQENGRWEAPQISCVPRRPARALHPEEDPEGRQGRLLGRWKAL
LIPPSSPMPGP

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-15
**N-glycosylation sites:**
Amino acids 130-134;337-341
**Tyrosine kinase phosphorylation sites:**
Amino acids 128-136;451-460
**N-myristoylation sites:**
Amino acids 47-53;50-56;133-139;142-148;
174-180;183-189;281-287;288-294;
297-303;324-330;403-409;414-420;
415-421;576-582;586-592;677-683;
684-690;720-726;772-778;811-817
**EGF-like domain cysteine pattern signature:**
Amino acids 670-682
**C-type lectin domain signature:**
Amino acids 784-809
**Immunoglobulins and major histocompatibility complex proteins signature:**
Amino acids 135-142
**Link domain proteins:**
Amino acids 166-216;264-314
**Calcium-binding EGF-like domain proteins pattern proteins.**
Amino acids 655-676
**C-type lectin domain proteins:**
Amino acids 791-800

# FIGURE 53

CTGCCAGGTGACAGCCGCCAAGATGGGGTCTTGGGCCCTGCTGTGGCCTCCCCTGCTGTTCACCGGGCTGCTCG
TCCGACCCCCGGGGACCATGGCCCAGGCCCAGTACTGCTCTGTGAACAAGGACATCTTTGAAGTAGAGGAGAAC
ACAAATGTCACCGAGCCGCTGGTGGACATCCACGTCCCGGAGGGCCAGGAGGTGACCCTCGGAGCCTTGTCCAC
CCCCTTTGCATTTCGGATCCAGGGAAACCAGCTGTTTCTCAACGTGACTCCTGATTACGAGGAGAAGTCACTGC
TTGAGGCTCAGCTGCTGTGTCAGAGCGGAGGCACATTGGTGACCCAGCTAAGGGTGTTCGTGTCAGTGCTGGAC
GTCAATGACAATGCCCCCGAATTCCCCTTTAAGACCAAGGAGATAAGGGTGGAGGAGGACACGAAAGTGAACTC
CACCGTCATCCCTGAGACGCAACTGCAGGCTGAGGACCGCGACAAGGACGACATTCTGTTCTACACCCTCCAGG
AAATGACAGCAGGTGCCAGTGACTACTTCTCCCTGGTGAGTGTAAACCGTCCCGCCCTGAGGCTGGACCGGCCC
CTGGACTTCTACGAGCGGCCGAACATGACCTTCTGGCTGCTGGTGCGGGACACTCCAGGGGAGAATGTGGAACC
CAGCCACACTGCCACCGCCACACTAGTGCTGAACGTGGTGCCCGCCGACCTGCGGCCCCCGTGGTTCCTGCCCT
GCACCTTCTCAGATGGCTACGTCTGCATTCAAGCTCAGTACCACGGGGCTGTCCCCACGGGGCACATACTGCCA
TCTCCCCTCGTCCTGCGTCCCGGACCCATCTACGCTGAGGACGGAGACCGCGGCATCAACCAGCCCATCATCTA
CAGCATCTTTAGGGGAAACGTGAATGGTACATTCATCATCCACCCAGACTCGGGCAACCTCACCGTGGCCAGGA
GTGTCCCCAGCCCCATGACCTTCCTTCTGCTGGTGAAGGGCCAACAGGCCGACCTTGCCCGCTACTCAGTGACC
CAGGTCACCGTGGAGGCTGTGGCTGCGGCCGGGAGCCCGCCCCGCTTCCCCCAGAGCCTGTATCGTGGCACCGT
GGCGCGTGGCGCTGGAGCGGGCGTTGTGGTCAAGGATGCAGCTGCCCCTTCTCAGCCTCTGAGGATCCAGGCTC
AGGACCCGGAGTTCTCGGACCTCAACTCGGCCATCACATATCGAATTACCAACCACTCACACTTCCGGATGGAG
GGAGAGGTTGTGCTGACCACCACCACACTGGCACAGGCGGGAGCCTTCTACGCAGAGGTTGAGGCCCACAACAC
GGTGACCTCTGGCACCGCAACCACAGTCATTGAGATACAAGTTTCCGAACAGGAGCCCCCCTCCACAGAGGCTG
GAGGAACAACTGGGCCCTGGACCAGCACCACTTCCGAGGTCCCCAGACCCCCTGAGCCCTCCCAGGGACCCTCC
ACGACCAGCTCTGGGGGAGGCACAGGCCCTCATCCACCCTCTGGCACAACTCTGAGGCCACCAACCTCGTCCAC
ACCCGGGGGGCCCCCGGGTGCAGAAAACAGCACCTCCCACCAACCAGCCACTCCCGGTGGGGACACAGCACAGA
CCCCAAAGCCAGGAACCTCTCAGCCGATGCCCCCCGGTGTGGGAACCAGCACCTCCCACCAACCAGCCACACCC
AGTGGGGGCACAGCACAGACCCCAGAGCCAGGAACCTCTCAGCCGATGCCCCCCAGTATGGGAACCAGCACCTC
CCACCAACCAGCCACACCCGGTGGGGGCACAGCACAGACCCCAGAGGCAGGAACCTCTCAGCCGATGCCCCCCG
GTATGGGAACCAGCACCTCCCACCAACCAACCACACCCGGTGGGGGCACAGCACAGACCCCAGAGCCAGGAACC
TCTCAGCCGATGCCCCTCAGCAAGAGCACCCCATCTTCAGGTGGCGGCCCCTCGGAGGACAAGCGCTTCTCGGT
GGTGGATATGGCGGCCCTGGGCGGGGTGCTGGGTGCGCTGCTGCTGCTGGCTCTCCTTGGCCTCGCCGTCCTTG
TCCACAAGCACTATGGCCCCCGGCTCAAGTGCTGCTCTGGCAAAGCTCCGGAGCCCCAGCCCCAAGGCTTTGAC
AACCAGGCGTTCCTCCCTGACCACAAGGCCAACTGGGCGCCCGTCCCCAGCCCCACGCACGACCCCAAGCCCGC
GGAGGCACCGATGCCCGCAGAGCCCGCACCCCCCGGCCCTGCCTCCCCAGGCGGTGCCCCTGAGCCCCCCGCAG
CGGCCCGAGCTGGCGGAAGCCCCACGGCGGTGAGGTCCATCCTGACCAAGGAGCGGCGGCCGGAGGGCGGGTAC
AAGGCCGTCTGGTTTGGCGAGGACATCGGGACGGAGGCAGACGTGGTCGTTCTCAACGCGCCCACCCTGGACGT
GGATGGCGCCAGTGACTCCGGCAGCGGCGACGAGGGCGAGGGCGCGGGGAGGGGTGGGGGTCCCTACGATGCAC
CCGGTGGTGATGACTCCTACATCTAAGTGGCCCCTCCACCCTCTCCCCCAGCCGCACGGGCACTGGAGGTCTCG
CTCCCCCAGCCTCCGACCCGAGGCAGAATAAAGCAAGGCTCCCGAAACCCAGGCCATGGCGTGGGGCAGGCGCG
TGGGTCCCTGGGGGCCCCATTCACTCAGTCCCCTGTCGTCATTAGCGCTTGAGCCCAGGTGTGCAGATGAGGCG
GTGGGTCTGGCCACGCTGTCCCCACCCCAAGGCTGCAGCACTTCCCGTAAACCACCTGCAGTGCCCGCCGCCTT
CCCGAGGCTCTGTGCCAGCTAGTCTGGGAAGTTCCTCTCCCGCTCTAACCACAGCCCGAGGGGGGCTCCCCTCC
CCCGACCTGCACCAGAGATCTCAGGCACCCGGCTCAACTCAGACCTCCCGCTCCCGACCCTACACAGAGATTGC
CTGGGGAGGCTGAGGAGCCGATGCAAACCCCCAAGGCGACGCACTTGGGAGCCGGTGGTCTCAAACACCTGCCG
GGGGTCCTAGTCCCCTTCTGAAATCTACATGCTTGGGTTGGAGCGCAGCAGTAAACACCCTGCCCAGTGACCTG
GACTGAGGCGCGCTGGGGGTGGGTGCGCCGTGTGGCCTGAGCAGGAGCCAGACCAGGAGGCCTAGGGGTGAGAG
ACACATTCCCCTCGCTGCTCCCAAAGCCAGAGCCCAGGCTGGGCGCCCATGCCCAGAACCATCAAGGGATCCCT
TGCGGCTTGTCAGCACTTTCCCTAATGGAAATACACCATTAATTCCTTTCCAAATGTTTT

# FIGURE 54

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA102846
><subunit 1 of 1, 839 aa, 1 stop
><MW: 87546, pI: 4.84, NX(S/T): 8
MGSWALLWPPLLFTGLLVRPPGTMAQAQYCSVNKDIFEVEENTNVTEPLVDIHVPEGQEV
TLGALSTPFAFRIQGNQLFLNVTPDYEEKSLLEAQLLCQSGGTLVTQLRVFVSVLDVNDN
APEFPFKTKEIRVEEDTKVNSTVIPETQLQAEDRDKDDILFYTLQEMTAGASDYFSLVSV
NRPALRLDRPLDFYERPNMTFWLLVRDTPGENVEPSHTATATLVLNVVPADLRPPWFLPC
TFSDGYVCIQAQYHGAVPTGHILPSPLVLRPGPIYAEDGDRGINQPIIYSIFRGNVNGTF
IIHPDSGNLTVARSVPSPMTFLLLVKGQQADLARYSVTQVTVEAVAAAGSPPRFPQSLYR
GTVARGAGAGVVVKDAAAPSQPLRIQAQDPEFSDLNSAITYRITNHSHFRMEGEVVLTTT
TLAQAGAFYAEVEAHNTVTSGTATTVIEIQVSEQEPPSTEAGGTTGPWTSTTSEVPRPPE
PSQGPSTTSSGGGTGPHPPSGTTLRPPTSSTPGGPPGAENSTSHQPATPGGDTAQTPKPG
TSQPMPPGVGTSTSHQPATPSGGTAQTPEPGTSQPMPPSMGTSTSHQPATPGGGTAQTPE
AGTSQPMPPGMGTSTSHQPTTPGGGTAQTPEPGTSQPMPLSKSTPSSGGGPSEDKRFSVV
DMAALGGVLGALLLLALLGLAVLVHKHYGPRLKCCSGKAPEPQPQGFDNQAFLPDHKANW
APVPSPTHDPKPAEAPMPAEPAPPGPASPGGAPEPPAAARAGGSPTAVRSILTKERRPEG
GYKAVWFGEDIGTEADVVVLNAPTLDVDGASDSGSGDEGEGAGRGGGPYDAPGGDDSYI

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-25

**Transmembrane domain:**
Amino acids 662-684

**N-glycosylation sites:**
Amino acids 44-48;140-144;198-202;297-301;
308-312;405-409;520-524

**Glycosaminoglycan attachment sites:**
Amino acids 490-494;647-651;813-817

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 655-659

**Tyrosine kinase phosphorylation sites:**
Amino acids 154-163;776-783

**N-myristoylation sites:**
Amino acids 57-63;102-108;255-261;294-300;
366-372;426-432;441-447;513-519;
517-523;530-536;548-554;550-556;
581-587;592-598;610-616;612-618;
623-629;648-654;666-672;667-673;
762-768;763-769;780-786;809-815;
821-827;833-839

**Cadherins extracellular repeated domain signature:**
Amino acids 112-123

# FIGURE 55

GCAGCTGGGTTCTCCCGGTTCCCTTGGGCAGGTGCAGGGTCGGGTTCAAAGCCTCCGGAACGCGTTTTGGCCTG
ATTTGAGGAGGGGGGCGGGGAGGGACCTGCGGCTTGCGGCCCCGCCCCCTTCTCCGGCTCGCAGCCGACCGGTA
AGCCCGCCTCCTCCCTCGGCCGGCCCTGGGGCCGTGTCCGCCGGGCAACTCCAGCCGAGGCCTGGGCTTCTGCC
TGCAGGTGTCTGCGGCGAGGCCCCTAGGGTACAGCCCGATTTGGCCCCATGGTGGGTTTCGGGGCCAACCGGCG
GGCTGGCCGCCTGCCCTCTCTCGTGCTGGTGGTGCTGCTGGTGGTGATCGTCGTCCTCGCCTTCAACTACTGGA
GCATCTCCTCCCGCCACGTCCTGCTTCAGGAGGAGGTGGCCGAGCTGCAGGGCCAGGTCCAGCGCACCGAAGTG
GCCCGCGGGCGGCTGGAAAAGCGCAATTCGGACCTCTTGCTGTTGGTGGACACGCACAAGAAACAGATCGACCA
GAAGGAGGCCGACTACGGCCGCCTCAGCAGCCGGCTGCAGGCCAGAGAGGGCCTCGGGAAGAGATGCGAGGATG
ACAAGGTTAAACTACAGAACAACATATCGTATCAGATGGCAGACATACATCATTTAAAGGAGCAACTTGCTGAG
CTTCGTCAGGAATTTCTTCGACAAGAAGACCAGCTTCAGGACTATAGGAAGAACAATACTTACCTTGTGAAGAG
GTTAGAATATGAAAGTTTTCAGTGTGGACAGCAGATGAAGGAATTGAGAGCACAGCATGAAGAAAATATTAAAA
AGTTAGCAGACCAGTTTTTAGAGGAACAAAAGCAAGAGACCCAAAAGATTCAATCAAATGATGGAAAGGAATTG
GATATAAACAATCAAGTAGTACCTAAAAATATTCCAAAAGTAGCTGAGAATGTTGCAGATAAGAATGAAGAACC
CTCAAGCAATCATATTCCACATGGGAAAGAACAAATCAAAAGAGGTGGTGATGCAGGGATGCCTGGAATAGAAG
AGAATGACCTAGCAAAAGTTGATGATCTTCCCCCTGCTTTAAGGAAGCCTCCTATTTCAGTTTCTCAACATGAA
AGTCATCAAGCAATCTCCCATCTTCCAACTGGACAACCTCTCTCCCCAAATATGCCTCCAGATTCACACATAAA
CCACAATGGAAACCCCGGTACTTCAAAACAGAATCCTTCCAGTCCTCTTCAGCGTTTAATTCCAGGCTCAAACT
TGGACAGTGAACCCAGAATTCAAACAGATATACTAAAGCAGGCTACCAAGGACAGAGTCAGTGATTTCCATAAA
TTGAAGCAAAATGATGAAGAACGAGAGCTTCAAATGGATCCTGCAGACTATGGAAAGCAACATTTCAATGATGT
CCTTTAAGTCCTAAAGGAATGCTTCAGAAAACCTAAAGTGCTGTAAAATGAAATCATTCTACTTTGTCCTTTCT
GACTTTTGTTGTAAAGACGAATTGTATCAGTTGTAAAGATACATTGAGATAGAATTAAGGAAAAACTTTAATGA
AGGAATGTACCCATGTACATATGTGAACTTTTTCATATTGTATTATCAAGGTATAGACTTTTTTGGTTATGATA
CAGTTAAGCCAAAAACAGCTAATCTTTGCATCTAAAGCAAACTAATGTATATTTCACATTTTATTGAGCCGACT
TATTTCCACAAATAGATAAACAGGACAAAATAGTTGTACAGGTTATATGTGGCATAGCATAACCACAGTAAGAA
CAGAACAGATATTCAGCAGAAAACTTTTTATACTCTAATTCTTTTTTTTTTTTTTTGAGACAGAGTTTTAGTC
TTGTTTCCCAGGCTGGAGTGCAATGGCACAATCTTGGCTCACTGCAACCTCCGCCTCCTGGGTTCAGGCAATTT
TCCTGCCTCAGCCTCCCAAGTAGCTGGGATTACAGGCACCCACCACCATGCCCAGCTAATTTTTGTATTTTTAA
TAGAGAGCTAATAATTGTATATTTAATAAAGACGGGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGAC
CTCAGGTGATCCTCCTGCATTGGCCTCCCAAAGTGCTGGAATTCCAGGCATGAGCCACTGCGCCCAGTCTACAC
ACTAATTCTTGTTAGCCCAACAGCTGTTCTGTTCTATCTACCCCTCATTTCACGCTCAAGGAGTCATACCTAGA
ATAGTTACACACAAGAGGGAAACTGGAAGCCAAACACTGTACAGTATTGTGTAGAAAGTCACCTCCCTACTCCT
TTTATTTTACATGAGTGCTGATGTGTTTTGGCAGATGAGCTTTCAGCTGAGGCCTGATGGAAATTGAGATAACCTG
CAAAGACATAACAGTATTTATGAGTTATATCTTAGTTCTTGAAATTGTGGAATGCATGATTGACAATATATTTT
TAATTTTTATTTTTTCAAGTAATACCAGTACTGTTTAACTATAGCCAGAACTGGCTAAAATTTTTATATTTTCA
GAGTTGAAGTTGGTGAAGACATTCATGATTTAAACACCAGATCCTGAAAGGGGTTAAATCTACTTTGAAATGAA
TCTGCAATCAGTATTTCAAAGCTTTTCTGGTAATTTTAGTGATCTTATTTGATTAGACTTTTTCAGAAGTACTA
AATAAGGAATTTTAACAGGTTTTTATTAATGCACAGATAAATAGAAGTACAGTGAGGTCTATAGCCATTTTATT
AAAATAGCTTAAAAGTTTGTAAAAAAATGAATCTTTGTAATTACTTAATATGTTAGTTAAGAACCCGTCAAGCT
TATATTTGCTAGACTTACAAATTATTTTAAATGCATTTATCTTTTTTGACACTATTCAGTGGAATGTGTAAGCT
AGCTAATTCTTGTTTTCTGATTTAAAGCACTTTTAAATCTTATCCTGCCCCCTAAAAACAAAAGGTTTTGATCA
CAAGGGGAAATTTAAGATTGTTAACCCTGTTTTTCAGAAGGGCTACTGTTAATTGCACATAAACATGAAATGTG
TTTTCCCCTGTGTACTAACACATTCTAGGCAAAATTCAAACTTATAGTGGTAAAGAAACAGGTTGTTCACTTGC
TGAGGTGCAAAAATTCTTAAGACTTCTGTTTGAAATTGCTCAATGACTAGGAAAAGATGTAGTAGTTTACTAAA
ATTGTTTTTCTACCATATCAAATTAAACAATTCATGCCTTTATAGGGTCAGGCCTACAATGAATAGGTATGGTG
GTTTCACAGAATTTTAAAATAGAGTTAAAGGGAAGTGATGTACATTTCGGGGGCATTAGGGTAGGGAGATGAAT
CAAAAAATACCCCTAGTAATGCTTTATATTTTAATACTGCAAAAGCTTTACAAATGGAAACCATGCAATTACCT
GCCTTAGTTCTTTTGTCATAAAAACAATCACTTGGTTGGTTGTATTGTAGCTATTACTTATACAGCAACATTTC
TTCAATTAGCAGTCTAGACATTTTATAAACAGAAATCTTGGACCAATTGATAATATTTCTGACTGTATTAATAT
TTTAGTGCTATAAAATACTATGTGAATCTCTTAAAAATCTGACATTTTACAGTCTGTATTAGACATACTGTTTTTA
TAATGTTTTACTTCTGCCTTAAGATTTAGGTTTTTTAAATGTATTTTTGCCCTGAATTAAGTGTTAATTTGATG
GAAACTCTGCTTTTAAAATCATCATTTACTGGGTTCTAATAAATTAAAAATTAAACTTGAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 56

MVGFGANRRAGRLPSLVLVVLLVVIVVLAFNYWSISSRHVLLQEEVAELQGQVQRTEVAR
GRLEKRNSDLLLLVDTHKKQIDQKEADYGRLSSRLQAREGLGKRCEDDKVKLQNNISYQM
ADIHHLKEQLAELRQEFLRQEDQLQDYRKNNTYLVKRLEYESFQCGQQMKELRAQHEENI
KKLADQFLEEQKQETQKIQSNDGKELDINNQVVPKNIPKVAENVADKNEEPSSNHIPHGK
EQIKRGGDAGMPGIEENDLAKVDDLPPALRKPPISVSQHESHQAISHLPTGQPLSPNMPP
DSHINHNGNPGTSKQNPSSPLQRLIPGSNLDSEPRIQTDILKQATKDRVSDFHKLKQNDE
ERELQMDPADYGKQHFNDVL

**Important features of the protein:**
**Signal peptide:**
1-29

**Transmembrane domain.**
None

**N-glycosylation site.**
115-119
150-154

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**
65-69

**N-myristoylation site.**
246-252
253-259
308-314

**Amidation site.**
101-105

# FIGURE 57

GGATGGGCGAGCAGTCTGAATGCCAGAATGGATAACCGTTTTGCTACAGCATTTGTAATTGC
TTGTGTGCTTAGCCTCATTTCCACCATCTACATGGCAGCCTCCATTGGCACAGACTTCTGGT
ATGAATATCGAAGTCCAGTTCAAGAAAATTCCAGTGATTTGAATAAAAGCATCTGGGATGAA
TTCATTAGTGATGAGGCAGATGAAAAGACTTATAATGATGCACTTTTTCGATACAATGGCAC
AGTGGGATTGTGGAGACGGTGTATCACCATACCCAAAAACATGCATTGGTATAGCCCACCAG
AAAGGACAGAGTCATTTGATGTGGTCACAAAATGTGTGAGTTTCACACTAACTGAGCAGTTC
ATGGAGAAATTTGTTGATCCCGGAAACCACAATAGCGGGATTGATCTCCTTAGGACCTATCT
TTGGCGTTGCCAGTTCCTTTTACCTTTTGTGAGTTTAGGTTTGATGTGCTTTGGGGCTTTGA
TCGGACTTTGTGCTTGCATTTGCCGAAGCTTATATCCCACCATTGCCACGGGCATTCTCCAT
CTCCTTGCAGATACCATGCTGTGAAGTCCAGGCCACATGGAGGTGTCCTGTGTAGATGCTCC
AGCTGAAATCCCAAGCTAAGCTCCCAACTGACAGCCAACATCATTTCCAGCCATGTGTGGGA
GCCATCCTGGATGTCCAGCCTTAACAAGCCTTCAGAGGACTTCAGCCACAGCTATTATCTTA
CTACATCCTTGTGAGACTCTAATAAAGAACCAACTAGCTGAGCCCAATCAACCTATGGAACTG
ATAGAAATAAAATGAATTGTTGTTTTGTGCCGTT

# FIGURE 58

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA102880
><subunit 1 of 1, 184 aa, 1 stop
><MW: 21052, pI: 5.01, NX(S/T): 3
MDNRFATAFVIACVLSLISTIYMAASIGTDFWYEYRSPVQENSSDLNKSIWDEFISDEAD
EKTYNDALFRYNGTVGLWRRCITIPKNMHWYSPPERTESFDVVTKCVSFTLTEQFMEKFV
DPGNHNSGIDLLRTYLWRCQFLLPFVSLGLMCFGALIGLCACICRSLYPTIATGILHLLA
DTML

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-20

**Transmembrane domain:**
Amino acids 142-163

**N-glycosylation sites:**
Amino acids 42-46;47-51;72-76;

**N-myristoylation sites:**
Amino acids 123-129;154-160;158-164

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 152-163

# FIGURE 59

GCGTGGACACCACCTCAGCCCACTGAGCAGGAGTCACAGCACGAAGACCAAGCGCAAAGCGA
CCCCTGCCCTCCATCCTGACTGCTCCTCCTAAGAGAGATGGCACCGGCCAGAGCAGGATTCT
GCCCCCTTCTGCTGCTTCTGCTGCTGGGGCTGTGGGTGGCAGAGATCCCAGTCAGTGCCAAG
CCCAAGGGCATGACCTCATCACAGTGGTTTAAAATTCAGCACATGCAGCCCAGCCCTCAAGC
ATGCAACTCAGCCATGAAAAACATTAACAAGCACACAAAACGGTGCAAAGACCTCAACACCT
TCCTGCACGAGCCTTTCTCCAGTGTGGCCGCCACCTGCCAGACCCCCAAAATAGCCTGCAAG
AATGGCGATAAAAACTGCCACCAGAGCCACGGGCCCGTGTCCCTGACCATGTGTAAGCTCAC
CTCAGGGAAGTATCCGAACTGCAGGTACAAAGAGAAGCGACAGAACAAGTCTTACGTAGTGG
CCTGTAAGCCTCCCCAGAAAAAGGACTCTCAGCAATTCCACCTGGTTCCTGTACACTTGGAC
AGAGTCCTTTAGGTTTCCAGACTGGCTTGCTCTTTGGCTGACCTTCAATTCCCTCTCCAGGA
CTCCGCACCACTCCCCTACACCCAGAGCATTCTCTTCCCCTCATCTCTTGGGGCTGTTCCTG
GTTCAGCCTCTGCTGGGAGGCTGAAGCTGACACTCTGGTGAGCTGAGCTCTAGAGGGATGGC
TTTTCATCTTTTTGTTGCTGTTTTCCCAGATGCTTATCCCCAAGAAACAGCAAGCTCAGGTC
TGTGGGTTCCCTGGTCTATGCCATTGCACATGTCTCCCCTGCCCCCTGGCATTAGGGCAGCA
TGACAAGGAGAGGAAATAAATGGAAAGGGGGCAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAA

# FIGURE 60

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA105782
><subunit 1 of 1, 156 aa, 1 stop
><MW: 17472, pI: 10.01, NX(S/T): 1
MAPARAGFCPLLLLLLLGLWVAEIPVSAKPKGMTSSQWFKIQHMQPSPQACNSAMKNINK
HTKRCKDLNTFLHEPFSSVAATCQTPKIACKNGDKNCHQSHGPVSLTMCKLTSGKYPNCR
YKEKRQNKSYVVACKPPQKKDSQQFHLVPVHLDRVL

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-22

**N-glycosylation site:**
Amino acids 127-131

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 139-143

**N-myristoylation sites:**
Amino acids 18-24;32-38

**Pancreatic ribonuclease family signature:**
Amino acids 65-72

**Pancreatic ribonuclease family proteins:**
Amino acids 49-93

# FIGURE 61

CGGGTC**ATG**CGCCGCCGCCTGTGGCTGGGCCTGGCCTGGCTGCTGCTGGCGCGGGCGCCGGA
CGCCGCGGGAACCCCGAGCGCGTCGCGGGGACCGCGCAGCTACCCGCACCTGGAGGGCGACGTG
CGCTGGCGGCGCCTCTTCTCCTCCACTCACTTCTTCCTGCGCGTGGATCCCGGCGGCCGCGT
GCAGGGCACCCGCTGGCGCCACGGCCAGGACAGCATCCTGGAGATCCGCTCTGTACACGTGG
GCGTCGTGGTCATCAAAGCAGTGTCCTCAGGCTTCTACGTGGCCATGAACCGCCGGGGCCGC
CTCTACGGGTCGCGACTCTACACCGTGGACTGCAGGTTCCGGGAGCGCATCGAAGAGAACGG
CCACAACACCTACGCCTCACAGCGCTGGCGCCGCCGCGGCCAGCCCATGTTCCTGGCGCTGG
ACAGGAGGGGGGGGCCCCGGCCAGGCGGCCGGACGCGGCGGTACCACCTGTCCGCCCACTTC
CTGCCCGTCCTGGTCTCC**TGA**G

# FIGURE 62

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA108912
><subunit 1 of 1, 170 aa, 1 stop
><MW: 19663, pI: 11.81, NX(S/T): 0
MRRRLWLGLAWLLLARAPDAAGTPSASRGPRSYPHLEGDVRWRRLFSSTHFFLRVDPGGR
VQGTRWRHGQDSILEIRSVHVGVVVIKAVSSGFYVAMNRRGRLYGSRLYTVDCRFRERIE
ENGHNTYASQRWRRRGQPMFLALDRRGGPRPGGRTRRYHLSAHFLPVLVS

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-17

**N-myristoylation site:**
Amino acids 22-28

**HBGF/FGF family proteins:**
Amino acids 74-125;139-166

# FIGURE 63

ATCCCTCGACCTCGACCCACGCGTCCGCTGGAAGGTGGCGTGCCCTCCTCTGGCTGGTACCA
TGCAGCTCCCACTGGCCCTGTGTCTCGTCTGCCTGCTGGTACACACAGCCTTCCGTGTAGTG
GAGGGCCAGGGGTGGCAGGCGTTCAAGAATGATGCCACGGAAATCATCCCCGAGCTCGGAGA
GTACCCCGAGCCTCCACCGGAGCTGGAGAACAACAAGACCATGAACCGGGCGGAGAACGGAG
GGCGGCCTCCCCACCACCCCTTTGAGACCAAAGACGTGTCCGAGTACAGCTGCCGCGAGCTG
CACTTCACCCGCTACGTGACCGATGGGCCGTGCCGCAGCGCCAAGCCGGTCACCGAGCTGGT
GTGCTCCGGCCAGTGCGGCCCGGCGCGCCTGCTGCCCAACGCCATCGGCCGCGGCAAGTGGT
GGCGACCTAGTGGGCCCGACTTCCGCTGCATCCCCGACCGCTACCGCGCGCAGCGCGTGCAG
CTGCTGTGTCCCGGTGGTGAGGCGCCGCGCGCGCGCAAGGTGCGCCTGGTGGCCTCGTGCAA
GTGCAAGCGCCTCACCCGCTTCCACAACCAGTCGGAGCTCAAGGACTTCGGGACCGAGGCCG
CTCGGCCGCAGAAGGGCCGGAAGCCGCGGCCCCGCGCCCGGAGCGCCAAAGCCAACCAGGCC
GAGCTGGAGAACGCCTACTAGAGCCCGCCCGCGCCCCTCCCCACCGGCGGGCGCCCCGGCCC
TGAACCCGCGCCCCACATTTCTGTCCTCTGCGCGTGGTTTGATTGTTTATATTTCATTGTAA
ATGCCTGCAACCCAGGGCAGGGGGCTGAGACCTTCCAGGCCCTGAGGAATCCCGGGCGCCGG
CAAGGCCCCCCTCAGCCCGCCAGCTGAGGGGTCCCACGGGGCAGGGGAGGGAATTGAGAGTC
ACAGACACTGAGCCACGCAGCCCCGCCTCTGGGGCCGCCTACCTTTGCTGGTCCCACTTCAG
AGGAGGCAGAAATGGAAGCATTTTCACCGCCCTGGGGTTTTAAGGGAGCGGTGTGGGAGTGG
GAAAGTCCAGGGACTGGTTAAGAAAGTTGGATAAGATTCCCCCTTGCACCTCGCTGCCCATC
AGAAAGCCTGAGGCGTGCCCAGAGCACAAGACTGGGGGCAACTGTAGATGTGGTTTCTAGTCC
TGGCTCTGCCACTAACTTCCTGTGTAACCTTGAACTACACAATTCTCCTTCGGGACCTCAAT
TTCCACTTTGTAAAATGAGGGTGGAGGTGGGAATAGGATCTCGAGGAGACTATTGGCATATG
ATTCCAAGGACTCCAGTGCCTTTTGAATGGGCAGAGGTGAGAGAGAGAGAGAGAAAGAGAGA
GAATGAATGCAGTTGCATTGATTCAGTGCCAAGGTCACTTCCAGAATTCAGAGTTGTGATGC
TCTCTTCTGACAGCCAAAGATGAAAAACAAACAGAAAAAAAAAAAGTAAAGAGTCTATTTATG
GCTGACATATTTACGGCTGACAAACTCCTGGAAGAAGCTATGCTGCTTCCCAGCCTGGCTTC
CCCGGATGTTTGGCTACCTCCACCCCTCCATCTCAAAGAAATAACATCATCCATTGGGGTAG
AAAAGGAGAGGGTCCGAGGGTGGTGGGAGGGATAGAAATCACATCCGCCCCAACTTCCCAAA
GAGCAGCATCCCTCCCCCGACCCATAGCCATGTTTTAAAGTCACCTTCCGAAGAGAAGTGAA
AGGTTCAAGGACACTGGCCTTGCAGGCCCGAGGGAGCAGCCATCACAAACTCACAGACCAGC
ACATCCCTTTTGAGACACCGCCTTCTGCCCACCACTCACGGACACATTTCTGCCTAGAAAAC
AGCTTCTTACTGCTCTTACATGTGATGGCATATCTTACACTAAAAGAATATTATTGGGGGAA
AAACTACAAGTGCTGTACATATGCTGAGAAACTGCAGAGCATAATAGCTGCCACCCAAAAAT
CTTTTTGAAAATCATTTCCAGACAACCTCTTACTTTCTGTGTAGTTTTTAATTGTTAAAAAA
AAAAAGTTTTAAACAGAAGCACATGACATATGAAAGCCTGCAGGACTGGTCGTTTTTTTGGC
AATTCTTCCACGTGGGACTTGTCCACAAGAATGAAAGTAGTGGTTTTTAAAGAGTTAAGTTA
CATATTTATTTTCTCACTTAAGTTATTTATGCAAAAGTTTTTCTTGTAGAGAATGACAATGT
TAATATTGCTTTATGAATTAACAGTCTGTTCTTCCAGAGTCCAGAGACATTGTTAATAAAGA
CAATGAATCATGAAAAAAAAAAAAAAAAAAAAA

# FIGURE 64

</usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA115253
<subunit 1 of 1, 213 aa, 1 stop
<MW: 24031, pI: 9.59, NX(S/T): 2
MQLPLALCLVCLLVHTAFRVVEGQGWQAFKNDATEIIPELGEYPEPPPELENNKTMNRAE
NGGRPPHHPFETKDVSEYSCRELHFTRYVTDGPCRSAKPVTELVCSGQCGPARLLPNAIG
RGKWWRPSGPDFRCIPDRYRAQRVQLLCPGGEAPRARKVRLVASCKCKRLTRFHNQSELK
DFGTEAARPQKGRKPRPRARSAKANQAELENAY

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-16

**N-glycosylation sites:**
Amino acids 53-57;175-179

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 168-172

**N-myristoylation site:**
Amino acids 183-189

**Amidation site:**
Amino acids 191-195

# FIGURE 65

CCCACTCGGCGGTTTGGCGGGAGGGAGGGGCTTTGCGCAGGCCCCGCTCCCGCCCCGCCTCC
**ATG**CGGCCCGCCCCGATTGCGCTGTGGCTGCGCCTGGTCTTGGCCCTGGCCCTTGTCCGCCC
CCGGGCTGTGGGGTGGGCCCCGGTCCGAGCCCCCATCTATGTCAGCAGCTGGGCCGTCCAGG
TGTCCCAGGGTAACCGGGAGGTCGAGCGCCTGGCACGCAAATTCGGCTTCGTCAACCTGGGG
CCGATCTTCTCTGACGGGCAGTACTTTCACCTGCGGCACCGGGGCGTGGTCCAGCAGTCCCT
GACCCCGCACTGGGGCCACCGCCTGCACCTGAAGAAAAACCCCAAGGTGCAGTGGTTCCAGC
AGCAGACGCTGCAGCGGCGGGTGAAACGCTCTGTCGTGGTGCCCACGGACCCCTGGTTCTCC
AAGCAGTGGTACATGAACAGCGAGGCCCAACCAGACCTGAGCATCCTGCAGGCCTGGAGTCA
GGGGCTGTCAGGCCAGGGCATCGTGGTCTCTGTGCTGGACGATGGCATCGAGAAGGACCACC
CGGACCTCTGGGCCAACTACGACCCCCTGGCCAGCTATGACTTCAATGACTACGACCCGGAC
CCCCAGCCCCGCTACACCCCCAGCAAAGAGAACCGGCACGGGACCCGCTGTGCTGGGGAGGT
GGCCGCGATGGCCAACAATGGCTTCTGTGGTGTGGGGGTCGCTTTCAACGCCCGAATCGGAG
GCGTACGGATGCTGGACGGTACCATCACCGATGTCATCGAGGCCCAGTCGCTGAGCCTGCAG
CCGCAGCACATCCACATTTACAGCGCCAGCTGGGGTCCCGAGGACGACGGCCGCACGGTGGA
CGGCCCCGGCATCCTCACCCGCGAGGCCTTCCGGCGTGGTGTGACCAAGGGCCGCGGCGGGC
TGGGCACGCTCTTCATCTGGGCCTCGGGCAACGGCGGCCTGCACTACGACAACTGCAACTGC
GACGGCTACACCAACAGCATCCACACGCTTTCCGTGGGCAGCACCACCCAGCAGGGCCGCGT
GCCCTGGTACAGCGAAGCCTGCGCCTCCACCCTCACCACCACCTACAGCAGCGGCGTGGCCA
CCGACCCCCAGATCGTCACCACGGACCTGCATCACGGGTGCACAGACCAGCACACGGGCACC
TCGGCCTCAGCCCCACTGGCGGCCGGCATGATCGCCCTAGCGCTGGAGGCCAACCCGTTCCT
GACGTGGAGAGACATGCAGCACCTGGTGGTCCGCGCGTCCAAGCCGGCGCACCTGCAGGCCG
AGGACTGGAGGACCAACGGCGTGGGGCGCCAAGTGAGCCATCACTACGGATACGGGCTGCTG
GACGCCGGGCTGCTGGTGGACACCGCCCGCACCTGGCTGCCCACCCAGCCGCAGAGGAAGTG
CGCCGTCCGGGTCCAGAGCCGCCCCACCCCCATCCTGCCGCTGATCTACATCAGGGAAAACG
TATCGGCCTGCGCCGGCCTCCACAACTCCATCCGCTCGCTGGAGCACGTGCAGGCGCAGCTG
ACGCTGTCCTACAGCCGGCGCGGAGACCTGGAGATCTCGCTCACCAGCCCCATGGGCACGCG
CTCCACACTCGTGGCCATACGACCCTTGGACGTCAGCACTGAAGGCTACAACAACTGGGTCT
TCATGTCCACCCACTTCTGGGATGAGAACCCACAGGGCGTGTGGACCCTGGGCCTAGAGAAC
AAGGGCTACTATTTCAACACGGGGACGTTGTACCGCTACACGCTGCTGCTCTATGGGACGGC
CGAGGACATGACAGCGCGGCCTACAGGCCCCCAGGTGACCAGCAGCGCGTGTGTGCAGCGGGAC
ACAGAGGGGCTGTGCCAGGCGTGTGACGGCCCCGCCTACATCCTGGGACAGCTCTGCCTGGC
CTACTGCCCCCCGCGGTTCTTCAACCACACAAGGCTGGTGACCGCTGGGCCTGGGCACACGG
CGGCGCCCGCGCTGAGGGTCTGCTCCAGCTGCCATGCCTCCTGCTACACCTGCCGCGGCGGC
TCCCCGAGGGACTGCACCTCCTGTCCCCCATCCTCCACGCTGGACCAGCAGCAGGGCTCCTG
CATGGGACCCACCACCCCCGACAGCCGCCCCCGGCTTAGAGCTGCCGCCTGTCCCCACCACCG
CTGCCCAGCCTCGGCCATGGTGCTGAGCCTCCTGGCCGTGACCCTCGGAGGCCCCGTCCTCT
GCGGCATGTCCATGGACCTCCCACTATACGCCTGGCTCTCCCGTGCCAGGGCCACCCCCACC
AAACCCCAGGTCTGGCTGCCAGCTGGAACC**TGA**AGTTGTCAGCTCAGAAAGCGACCTTGCCC
CCGCCTGGGTCCCTGACAGGCACTGCTGCCATGCTGCCTCCCCAGGCTGGCCCCAGAGGAGC
GAGCACCAGCACCCGACGCCTGGCCTGCCAGGGATGGGCCCCGTGGAACCCCGAAGCCTGGC
GGGAGAGAGAGAGAGAAGTCTCCTCTGCATTTTGGGTTTGGGCAGGAGTGGGCTGGGGGG
AGAGGCTGGAGCACCCCAAAAGCCAGGGGAAAGTGGAGGGAGAGAAACGTGACACTGTCCGT
CTCGGGCACCGCGTCCAACCTCAGAGTTTGCAAATAAAGGTTGCTTAGAAGGTGAA

# FIGURE 66

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119302
><subunit 1 of 1, 755 aa, 1 stop
><MW: 82785, pI: 8.71, NX(S/T): 2
MRPAPIALWLRLVLALALVRPRAVGWAPVRAPIYVSSWAVQVSQGNREVERLARKFGFVN
LGPIFSDGQYFHLRHRGVVQQSLTPHWGHRLHLKKNPKVQWFQQQTLQRRVKRSVVVPTD
PWFSKQWYMNSEAQPDLSILQAWSQGLSGQGIVVSVLDDGIEKDHPDLWANYDPLASYDF
NDYDPDPQPRYTPSKENRHGTRCAGEVAAMANNGFCGVGVAFNARIGGVRMLDGTITDVI
EAQSLSLQPQHIHIYSASWGPEDDGRTVDGPGILTREAFRRGVTKGRGGLGTLFIWASGN
GGLHYDNCNCDGYTNSIHTLSVGSTTQQGRVPWYSEACASTLTTTYSSGVATDPQIVTTD
LHHGCTDQHTGTSASAPLAAGMIALALEANPFLTWRDMQHLVVRASKPAHLQAEDWRTNG
VGRQVSHHYGYGLLDAGLLVDTARTWLPTQPQRKCAVRVQSRPTPILPLIYIRENVSACA
GLHNSIRSLEHVQAQLTLSYSRRGDLEISLTSPMGTRSTLVAIRPLDVSTEGYNNWVFMS
THFWDENPQGVWTLGLENKGYYFNTGTLYRYTLLLYGTAEDMTARPTGPQVTSSACVQRD
TEGLCQACDGPAYILGQLCLAYCPPRFFNHTRLVTAGPGHTAAPALRVCSSCHASCYTCR
GGSPRDCTSCPPSSTLDQQQGSCMGPTTPDSRPRLRAAACPHHRCPASAMVLSLLAVTLG
GPVLCGMSMDLPLYAWLSRARATPTKPQVWLPAGT

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-21

**Transmembrane domain:**
Amino acids 706-730

**N-glycosylation sites:**
Amino acids 475-479;629-633

**Glycosaminoglycan attachment sites:**
Amino acids 148-152;298-302

**N-myristoylation sites:**
Amino acids 151-157;200-206;217-223;219-225;
282-288;288-294;371-377;432-438;
481-487;515-521;603-609

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 586-597

**Cell attachment sequence:**
Amino acids 503-506

**Serine proteases, subtilase family, aspartic acid active site:**
Amino acids 154-166

**Serine proteases, subtilase family, histidine active site:**
Amino acids 199-210

**Serine proteases, subtilase family, serine active site:**
Amino acids 371-382

**Cytochrome c family heme-binding site signature:**
Amino acids 649-655

# FIGURE 67

ATGAGGAAGCTCCAGGGCAGGATGGTTTACCTGCCTGGACAGCAAG**ATG**ATGGCTACACTAG
CCCCCATTCTCTGGGCGCCTGGATTTGCCCACCAGATCTCCTCACCTCTTGCCCTTCACCTC
CTGCTGTACCTACAAGGTCTCCCCGATTCTCATCTGCCCATAATCATGGACACAGCCCCAGG
ATGTGCAGGACTCTCAGGGACCATCTGGAGTTCCAGCTGGAATCTGGGCCTGGTGGAGTGGG
AGTGGGGCAGGGGCCTGCATTGGGCTGACTTAGAGAGCACAGTTATTCCATCCATATGGAAA
**TAA**ACATTTTGGATTCCTGATC

# FIGURE 68

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119536
><subunit 1 of 1, 88 aa, 1 stop
><MW: 9645, pI: 5.45, NX(S/T): 0
MMATLAPILWAPGFAHQISSPLALHLLLYLQGLPDSHLPIIMDTAPGCAGLSGTIWSSSW
NLGLVEWEWGRGLHWADLESTVIPSIWK

**Signal sequence:**
Amino acids 1-15

**N-myristoylation sites:**
Amino acids 32-38;50-56;53-59;72-78

# FIGURE 69

TTTGCAGTGGGGTCCTCCTCTGGCCTCCTGCCCCTCCTGCTGCTGCTGCTGCTTCCATTGCT
GGCAGCCCAGGGTGGGGGTGGCCTGCAGGCAGCGCTGCTGGCCCTTGAGGTGGGGCTGGTGG
GTCTGGGGGCCTCCTACCTGCTCCTTTGTACAGCCCTGCACCTGCCCTCCAGTCTTTTCCTA
CTCCTGGCCCAGGGTACCGCACTGGGGGCCGTCCTGGGCCTGAGCTGGCGCCGAGGCCTC**AT**
**G**GGTGTTCCCCTGGGCCTTGGAGCTGCCTGGCTCTTAGCTTGGCCAGGCCTAGCTCTACCTC
TGGTGGCTATGGCAGCGGGGGGCAGATGGGTGCGGCAGCAGGGCCCCCGGGTGCGCCGGGGC
ATATCTCGACTCTGGTTGCGGGTTCTGCTGCGCCTGTCACCCATGGCCTTCCGGGCCCTGCA
GGGCTGTGGGGCTGTGGGGGACCGGGGTCTGTTTGCACTGTACCCCAAAACCAACAAGGATG
GCTTCCGCAGCCGCCTGCCCGTCCCTGGGCCCCGGCGGCGTAATCCCCGCACCACCCAACAC
CCATTAGCTCTGTTGGCAAGGGTCTGGGTCCTGTGCAAGGGCTGGAACTGGCGTCTGGCACG
GGCCAGCCAGGGTTTAGCATCCCACTTGCCCCCGTGGGCCATCCACACACTGGCCAGCTGGG
GCCTGCTTCGGGGTGAACGGCCCACCCGAATCCCCCGGCTACTACCACGCAGCCAGCGCCAG
CTAGGGCCCCCTGCCTCCCGCCAGCCACTGCCAGGGACTCTAGCCGGGCGGAGGTCACGCAC
CCGCCAGTCCCGGGCCCTGCCCCCCTGGAGG**TAG**CTGACTCCAGCCCTTCCAGCCCAAATCT
AGAGCATTGAGCACTTTATCTCCCACGACTCAGTGAAGTTTCTCCAGTCCCTAGTCCTCTCT
TTTCACCCACCTTCCTCAGTTTGCTCACTTACCCCAGGCCCAGCCCTTCGGACCTCTAGACA
GGCAGCCTCCTCAGCTGTGGAGTCCAGCAGTCACTCTGTGTTCTCCTGGCGCTCCTCCCCTA
AGTTATTGCTGTTCGCCCGCTGTGTGTGCTCATCCTCACCCTCATTGACTCAGGCCTGGGGC
CAGGGGTGGTGGAGGGTGGGAAGAGTCATGTTTTTTTTCTCCTCTTTGATTTTGTTTTTCTG
TCTCCCTTCCAACCTGTCCCCTTCCCCCCACCAAAAAAAAXXXXXXXXXXXXXXXXXXXXXX
XXXXXXXXXXXXXAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 70

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA119542
><subunit 1 of 1, 197 aa, 1 stop
><MW: 21992, pI: 12.18, NX(S/T): 0
MGVPLGLGAAWLLAWPGLALPLVAMAAGGRWVRQQGPRVRRGISRLWLRVLLRLSPMAFR
ALQGCGAVGDRGLFALYPKTNKDGFRSRLPVPGPRRRNPRTTQHPLALLARVWVLCKGWN
WRLARASQGLASHLPPWAIHTLASWGLLRGERPTRIPRLLPRSQRQLGPPASRQPLPGTL
AGRRSRTRQSRALPPWR

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-21

**N-myristoylation sites:**
Amino acids 2-8;6-12;146-152;178-184

**Amidation site:**
Amino acids 181-185

# FIGURE 71

GTTTGGGGGTTGTTTGGGATTAGTGAAGCTACTGCCTTTGCCGCCAGCGCAGCCTCAGAGTT
TGATTATTTGCA**ATG**TCAGGCTTTGAAAACTTAAACACGGATTTCTACCAGACAAGTTACAG
CATCGATGATCAGTCACAGCAGTCCTATGATTATGGAGGAAGTGGAGGACCCTATAGCAAAC
AGTATGCTGGCTATGACTATTCGCAGCAAGGCAGATTTGTCCCTCCAGACATGATGCAGCCA
CAACAGCCATACACCGGGCAGATTTACCAGCCAACTCAGGCATATACTCCAGCTTCACCTCA
GCCTTTCTATGGAAACAACTTTGAGGATGAGCCACCTTTATTAGAAGAGTTAGGTATCAATTTT
GACCACATCTGGCAAAAAACACTAACAGTATTACATCCGTTAAAAGTAGCAGATGGCAGCAT
CATGAATGAAACTGATTTGGCAGGTCCAATGGTTTTTTGCCTTGCTTTTGGAGCCACATTGC
TACTGGCTGGCAAAATCCAGTTTGGCTATGTATACGGGATCAGTGCAATTGGATGTCTAGGA
ATGTTTTGTTTATTAAACTTAATGAGTATGACAGGTGTTTCATTTGGTTGTGTGGCAAGTGT
CCTTGGATATTGTCTTCTGCCCATGATCCTACTTTCCAGCTTTGCAGTGATATTTTCTTTGC
AAGGAATGGTAGGAATCATTCTCACTGCTGGGATTATTGGATGGTGTAGTTTTTCTGCTTCC
AAAATATTTATTTCTGCATTAGCCATGGAAGGACAGCAACTTTTAGTAGCATATCCTTGCGC
TTTGTTATATGGAGTCTTTGCCCTGATTTCCGTCTTT**TGA**AAATTTATCTGGGATGTGGACA
TCAGTGGGCCAGATGTACAAAAAGGACCTTGAACTCTTAAATTGGACCAGCAAACTGCTGCA
GCGCAACTCTCATGCAGATTTACATTTGACTGTTGGAGCAATGAAAGTAAACGTGTATCTCT
TGTTCATTTTTATAGAACTTTTGCATACTATATTGGATTTACCTGCGGTGTGACTAGCTTTA
AATGTTTGTGTTTATACAGATAAGAAATGCTATTTCTTTCTGGTTCCTGCAGCCATTGAAAA
ACCTTTTTCCTTGCAAATTATAATGTTTTTGATAGATTTTTATCAACTGTGGGAAACCAAAC
ACAAAGCTGATAACCTTTCTTAAAAACGACCCAGTCACAGTAAAGAAGACACAAGACGGCCG
GGCGTGGTAGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGGCGGATCACAAG
GGCAGGAGATCGAGACCATCCTGGTTAACACGGTGAAACCCCGACTCTACTAAAACTACAAA
AAAAATTAGCTGGGCGTGGTGGCGGGCGCCTGTAGTCCCAGCTACTCAGGAGGCTGAGGCAG
GAGAAGTGTGAACCCAGGAGGCGGAGCTTGCAGTGAGCCGAGATCACACCACTGCACTCCAT
CCAGCCTGGGTGACAGGGTGAGACTCTGTCTCAAAAAAAAAAAAAAAAAGGAGACACAAGACT
TACTGCAAAAATATTTTTCCAAGGATTTAGGAAAGAAAAATTGCCTTGTATTCTCAAGTCAG
GTAACTCAAAGCAAAAAAGTGATCCAAATGTAGAGTATGAGTTTGCACTCCAAAAATTTGAC
ATTACTGTAAATTATCTCATGGAATTTTTGCTAAAATTCAGAGATACGGGAAGTTCACAATC
TACCTCATTGTAGACATGAAATGCGAACACTTACTTACATATTAATGTTAACTCAACCTTAG
GGACCTGGAATGGTTGCATTAATGCTATAATCGTTGGATCGCCACATTTCCCAAAAATAATA
AAAAAATCACTAACCTTTTTTAAGGAAAATATTTAAAGTTTTACAAAATTCAATATTGCAAT
TATCAATGTAAAGTACATTTGAATGCTTATTAAAACTTTCCCAATTAATTTT

# FIGURE 72

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA143498
><subunit 1 of 1, 257 aa, 1 stop
><MW: 27989, pI: 4.16, NX(S/T): 1
MSGFENLNTDFYQTSYSIDDQSQQSYDYGGSGGPYSKQYAGYDYSQQGRFVPPDMMQPQQ
PYTGQIYQPTQAYTPASPQPFYGNNFEDEPPLLEELGINFDHIWQKTLTVLHPLKVADGS
IMNETDLAGPMVFCLAFGATLLLAGKIQFGYVYGISAIGCLGMFCLLNLMSMTGVSFGCV
ASVLGYCLLPMILLSSFAVIFSLQGMVGIILTAGIIGWCSFSASKIFISALAMEGQQLLV
AYPCALLYGVFALISVF

**Transmembrane domain:**
Amino acids 129-145;184-203

**N-glycosylation sites:**
Amino acids 123-127

**N-myristoylation sites:**
Amino acids 32-38;119-125;174-180;178-184;208-214

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 150-161;169-180

# FIGURE 73

ACACTGGCCAAAACGCGGCTCGCCCTCGGCTGCGCTCGGCTCCCGCGGGCGCTCGGCCCCGA
GCCCCTCCTCCCCCTACCCGCCGGCCGGACAGGGAGGAGCCA**ATG**GCTGGGCCTGCCATCCA
CACCGCTCCCATGCTGTTCCTCGTCCTCCTGCTGCCCCAGCTGAGCCTGGCAGGCGCCCTTG
CACCTGGGACCCCTGCCCGGAACCTCCCTGAGAATCACATTGACCTCCCAGGCCCAGCGCTG
TGGACGCCTCAGGCCAGCCACCACCGCCGGCGGGGCCCGGGCAAGAAGGAGTGGGGCCCAGG
CCTGCCCAGCCAGGCCCAGGATGGGGCTGTGGTCACCGCCACCAGGCAGGCCTCCAGGCTGC
CAGAGGCTGAGGGGCTGCTGCCTGAGCAGAGTCCTGCAGGCCTGCTGCAGGACAAGGACCTG
CTCCTGGGACTGGCATTGCCCTACCCCGAGAAGGAGAACAGACCTCCAGGTTGGGAGAGGAC
CAGGAAACGCAGCAGGGAGCACAAGAGACGCAGGGACAGGTTGAGGCTGCACCAAGGCCGAG
CCTTGGTCCGAGGTCCCAGCTCCCTGATGAAGAAGGCAGAGCTCTCCGAAGCCCAGGTGCTG
GATGCAGCCATGGAGGAATCCTCCACCAGCCTGGCGCCCACCATGTTCTTTCTCACCACCTT
TGAGGCAGCACCTGCCACAGAAGAGTCCCTGATCCTGCCCGTCACCTCCCTGCGGCCCCAGC
AGGCACAGCCCAGGTCTGACGGGGAGGTGATGCCCACGCTGGACATGGCCTTGTTCGACTGG
ACCGATTATGAAGACTTAAAACCTGATGGTTGGCCCTCTGCAAAGAAGAAAGAGAAACACCG
CGGTAAACTCTCCAGTGATGGTAACGAAACATCACCAGCCGAAGGGGAACCATGCGACCATC
ACCAAGACTGCCTGCCAGGGACTTGCTGCGACCTGCGGGAGCATCTCTGCACACCCCACAAC
CGAGGCCTCAACAACAAATGCTTCGATGACTGCATGTGTGTGGAAGGGCTGCGCTGCTATGC
CAAATTCCACCGGAACCGCAGGGTTACACGGAGGAAAGGGCGCTGTGTGGAGCCCGAGACGG
CCAACGGCGACCAGGGATCCTTCATCAACGTC**TAG**CGGCCCCGCGGGACTGGGGACTGAGCC
CAGGAGGTTTGCACAAGCCGGGCGATTTGTTTGTAACTAGCAGTGGGAGATCAAGTTGGGGA
ACAGATGGCTGAGGCTGCAGACTCAGGCCCAGGACACTCAACCCC

# FIGURE 74

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA145583
><subunit 1 of 1, 348 aa, 1 stop
><MW: 38536, pI: 8.24, NX(S/T): 1
MAGPAIHTAPMLFLVLLLPQLSLAGALAPGTPARNLPENHIDLPGPALWTPQASHHRRRG
PGKKEWGPGLPSQAQDGAVVTATRQASRLPEAEGLLPEQSPAGLLQDKDLLLGLALPYPE
KENRPPGWERTRKRSREHKRRRDRLRLHQGRALVRGPSSLMKKAELSEAQVLDAAMEESS
TSLAPTMFFLTTFEAAPATEESLILPVTSLRPQQAQPRSDGEVMPTLDMALFDWTDYEDL
KPDGWPSAKKKEKHRGKLSSDGNETSPAEGEPCDHHQDCLPGTCCDLREHLCTPHNRGLN
NKCFDDCMCVEGLRCYAKFHRNRRVTRRKGRCVEPETANGDQGSFINV

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-24

**N-glycosylation site:**
Amino acids 263-267

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 132-136;323-327

**N-myristoylation sites:**
Amino acids 77-83;343-349

**Amidation site:**
Amino acids 61-65

# FIGURE 75

CAGAAGGGCAAAAACATTGACTGCCTCAAGGTCTCAAGCACCAGTCTTCACCGCGGAAAGCA
TGTTGTGGCTGTTCCAATCGCTCCTGTTTGTCTTCTGCTTTGGCCCAGGGAATGTAGTTTCA
CAAAGCAGCTTAACCCCATTGATGGTGAACGGGATTCTGGGGGAGTCAGTAACTCTTCCCCT
GGAGTTTCCTGCAGGAGAGAAGGTCAACTTCATCACTTGGCTTTTCAATGAAACATCTCTTG
CCTTCATAGTACCCCATGAAACCAAAAGTCCAGAAATCCACGTGACTAATCCGAAACAGGGA
AAGCGACTGAACTTCACCCAGTCCTACTCCCTGCAACTCAGCAACCTGAAGATGGAAGACAC
AGGCTCTTACAGAGCCCAGATATCCACAAAGACCTCTGCAAAGCTGTCCAGTTACACTCTGA
GGATATTAAGACAACTGAGGAACATACAAGTTACCAATCACAGTCAGCTATTTCAGAATATG
ACCTGTGAGCTCCATCTGACTTGCTCTGTGGAGGATGCAGATGACAATGTCTCATTCAGATG
GGAGGCCTTGGGAAACACACTTTCAAGTCAGCCAAACCTCACTGTCTCCTGGGACCCCAGGA
TTTCCAGTGAACAGGACTACACCTGCATAGCAGAGAATGCTGTCAGTAATTTATCCTTCTCT
GTCTCTGCCCAGAAGCTTTGCGAAGATGTTAAAATTCAATATACAGATACCAAAATGATTCT
GTTTATGGTTTCTGGGATATGCATAGTCTTCGGTTTCATCATACTGCTGTTACTTGTTTTGA
GGAAAAGAAGAGATTCCCTATCTTTGTCTACTCAGCGAACACAGGGCCCCGCAGAGTCCGCA
AGGAACCTAGAGTATGTTTCAGTGTCTCCAACGAACAACACTGTGTATGCTTCAGTCACTCA
TTCAAACAGGGAAACAGAAATCTGGACACCTAGAGAAAATGATACTATCACAATTTACTCCA
CAATTAATCATTCCAAAGAGAGTAAACCCACTTTTTCCAGGGCAACTGCCCTTGACAATGTC
GTGTAAGTTGCTGAAAGGCCTCAGAGGAATTCGGGAATGACACGTCTTCTGATCCCATGAGA
CAGAACAAAGAACAGGAAGCTTGGTTCCTGTTGTTCCTGGCAACAGAATTTGAATATCTAGG
ATAGGATGATCACCTCCAGTCCTTCGGACTTAAACCTGCCTACCTGAGTCAAACACCTAAGG
ATAACATCATTTCCAGCATGTGGTTCAAATAATATTTTCCAATCCACTTCAGGCCAAAACAT
GCTAAAGATAACACACCAGCACATTGACTCTCTCTTTGATAACTAAGCAAATGGAATTATGG
TTGACAGAGAGTTTATGATCCAGAAGACAACCACTTCTCTCCTTTTAGAAAGCAGCAGGATT
GACTTATTGAGAAATAATGCAGTGTGTTGGTTACATGTGTAGTCTCTGGAGTTGGATGGGCC
CATCCTGATACAAGTTGAGCATCCCTTGTCTGAAATGCTTGGGATTAGAAATGTTTCAGATT
TCAATTTTTTTTCAGATTTTGGAATATTTGCATTATATTTAGCGGTTGAGTATCCAAATCCA
AAAATCCAAAATTCAAAATGCTCCAATAAGCATTTCCCTTGAGTTTCATTGATGTCGATGCA
GTGCTCAAAATCTCAGATTTTGGAGCAATTTGGATATTGGATTTTTGGATTTGGGATGCTCA
ACTTGTACAATGTTTATTAGACACATCTCCTGGGACATACTGCCTAACCTTTTGGAGCCTTA
GTCTCCCAGACTGAAAAAGGAAGAGGATGGTATTACATCAGCTCCATTGTTTGAGCCAAGAA
TCTAAGTC

# FIGURE 76

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA161000
><subunit 1 of 1, 332 aa, 1 stop
><MW: 37345, pI: 6.72, NX(S/T): 10
MLWLFQSLLFVFCFGPGNVVSQSSLTPLMVNGILGESVTLPLEFPAGEKVNFITWLFNET
SLAFIVPHETKSPEIHVTNPKQGKRLNFTQSYSLQLSNLKMEDTGSYRAQISTKTSAKLS
SYTLRILRQLRNIQVTNHSQLFQNMTCELHLTCSVEDADDNVSFRWEALGNTLSSQPNLT
VSWDPRISSEQDYTCIAENAVSNLSFSVSAQKLCEDVKIQYTDTKMILFMVSGICIVFGF
IILLLLVLRKRRDSLSLSTQRTQGPAESARNLEYVSVSPTNNTVYASVTHSNRETEIWTP
RENDTITIYSTINHSKESKPTFSRATALDNVV

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-13

**Transmembrane domain:**
Amino acids 228-247

**N-glycosylation sites:**
Amino acids 58-62;87-91;137-141;144-148;161-165;
178-182;203-207;281-285;303-307;
313-317

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 251-255

**Tyrosine kinase phosphorylation sites:**
Amino acids 100-108;186-194

**N-myristoylation sites:**
Amino acids 17-23;105-111;170-176

**Amidation site:**
Amino acids 82-86

**Immunoglobulin domain:**
Amino acids 35-111

# FIGURE 77

GATCCCTCGACCTCGACCCACGCGTCCGCTCTTTAATGCTTTCTTTTTAAGAGATCACCTTC
TGACTTCTCACAGAAGAGGTTAACTATTACCTGTGGGAAGTCAGAAGGTGATCTCTTTAATG
CTTTCTTTTTAAGAATTTTTCAAATTGAGACTAATTGCAGAGGTTCCAGTTGACCAGCATTC
ATAGGAATGAAGACAAACACAGAGATGGTGTGTCTAAGAAACTTCAAAAGGTGTAGACCTCC
TGACTGAAGCATATTGGATTTATTTAATTTTTTTCACTGTATTTCTGTCCTCCTACAAGGGA
AAGTCATGATTACACTAACTGAGCTAAAATGCTTAGCAGATGCCCAGTCATCTTATCACATC
TTAAAACCATGGTGGGACGTCTTCTGGTATTACATCACACTGATCATGCTGCTGGTGGCCGTG
CTGGCCGGAGCTCTCCAGCTGACGCAGAGCAGGGTTCTGTGCTGTCTTCCATGCAAAGTGGA
ATTTGACAATCACTGTGCCGTGCCTTGGGACATCCTGAAAGCCAGCATGAACACATCCTCTA
ATCCTGGGACACCGCTTCCGCTCCCCCTCCGAATTCAGAATGACCTCCACCGACAGCAGTAC
TCCTATATTGATGCCGTCTGTTACGAGAAACAGCTCCATTGGTTTGCAAAGTTTTTCCCCTA
TCTGGTGCTCTTGCACACGCTCATCTTTGCAGCCTGCAGCAACTTTTGGCTTCACTACCCCA
GTACCAGTTCCAGGCTCGAGCATTTTGTGGCCATCCTTCACAAGTGCTTCGATTCTCCATGG
ACCACCCGCGCCCTTTCAGAAACAGTGGCTGAGCAGTCAGTGAGGCCTCTGAAACTCTCCAA
GTCCAAGATTTTGCTTTCGTCCTCAGGGTGTTCAGCTGACATAGATTCCGGCAAACAGTCAT
TGCCCTACCCACAGCCAGGTTTGGAGTCAGCTGGTATAGAAAGCCCAACTTCCAGTGGCCTG
GACAAGAAGGAGGGTGAACAGGCCAAAGCCATCTTTGAAAAAGTGAAAAGATTCCGCATGCA
TGTGGAGCAGAAGGACATCATTTATAGAGTATATCTGAAACAGATAATAGTCAAAGTCATTT
TGTTTGTGCTCATCATAACTTATGTTCCATATTTTTTAACCCACATCACTCTTGAAATCGAC
TGTTCAGTTGATGTGCAGGCTTTTACAGGATATAAGCGCTACCAGTGTGTCTATTCCTTGGC
AGAAATCTTTAAGGTCCTGGCTTCATTTTATGTCATTTTGGTTATACTTTATGGTCTGACCT
CTTCCTACAGCCTGTGGTGGATGCTGAGGAGTTCCCTGAAGCAATATTCCTTTGAGGCGTTA
AGAGAAAAAAGCAACTACAGTGACATCCCTGATGTCAAGAATGACTTTGCCTTCATCCTTCA
TCTGGCTGATCAGTATGATCCTCTTTATTCCAAACGCTTCTCCATATTCCTATCAGAGGTCA
GTGAGAACAAACTGAAACAGATCAACCTCAATAATGAATGGACAGTTGAGAAACTGAAAAGT
AAGCTTGTGAAAAATGCCCAGGACAAGATAGAACTGCATCTTTTTATGCTCAACGGTCTTCC
AGACAATGTCTTTGAGTTAACTGAAATGGAAGTGCTAAGCCTGGAGCTTATCCCAGAGGTGA
AGCTGCCCTCTGCAGTCTCACAGCTGGTCAACCTCAAGGAGCTTCGTGTGTACCATTCATCT
CTGGTCGTAGACCATCCTGCACTGGCCTTTCTAGAGGAGAATTTAAAAATCCTCCGCCTGAA
ATTTACTGAAATGGGAAAAATCCCACGCTGGGTATTTCACCTCAAGAATCTCAAGGAACTTT
ATCTTTCGGGCTGTGTTCTCCCTGAACAGTTGAGTACTATGCAGTTGGAGGGCTTTCAGGAC
TTAAAAAATCTAAGGACCCTGTACTTGAAGAGCAGCCTCTCCCGGATCCCACAAGTTGTTACA
GACCTCCTGCCTTCATTGCAGAAACTGTCCCTTGATAATGAGGGAAGCAAACTGGTTGTGTT
GAACAACTTGAAAAAGATGGTCAATCTGAAAAGCCTAGAACTGATCAGCTGTGACCTGGAAC
GCATCCCACATTCCATTTTCAGCCTGAATAATTTGCATGAGTTAGACCTAAGGGAAAATAAC
CTTAAAACTGTGGAAGAGATTAGCTTTCAGCATCTTCAGAATCTTTCCTGCTTAAAGTTGTG
GCACAATAACATTGCTTATATTCCTGCACAGATTGGGGCATTATCTAACCTAGAGCAGCTCT
CTTTGGACCATAATAATATTGAGAATCTGCCCTTGCAGCTTTTCCTATGCACTAAACTACAT
TATTTGGATCTAAGCTATAACCACTTGACCTTCATTCCAGAAGAAATCCAGTATCTGAGTAA
TTTGCAGTACTTTGCTGTGACCAACAACAATATTGAGATGCTACCAGATGGGCTGTTTCAGT
GCAAAAAGCTGCAGTGTTTACTTTTGGGGAAAAATAGCTTGATGAATTTGTCCCCTCATGTG
GGTGAGCTGTCAAACCTTACTCATCTGGAGCTCATTGGTAATTACCTGGAAACACTTCCTCC
TGAACTAGAAGGATGTCAGTCCCTAAAACGGAACTGTCTGATTGTTGAGGAGAACTTGCTCA
ATACTCTTCCTCTCCCTGTAACAGAACGTTTACAGACGTGCTTAGACAAATGTTGACTTAAA
GAAAAGAGACCCGTGTTTCAAAATCATTTTTAAAAGTATGCTCGGCCGGGCGTGGTGGCTCA
TGCCTATAATCCCAGCACTTTGGGAGGCCAAGATGGGCGGATTGCTTGAGGTCAGGAGTTCG
AGACCAGTCTGGCCAACCTGGTGAAACCCCATCTCTGCTAAAACTACAAAAAAATTAGCCAG
GCGTGGTGGCGTGCGCCTGTAATCCCAGCTACTTGGGAGGCTGACGCAGGGGAATTGCTTGA
ACCAGGGAGGTGGAGGTTGCAGTGAGCCGAGATTGTGCCACTGTACACCAGCCTGGGTGACA
GAGCAAGACTCTTATCTCAAAAAAAAAAAAAAA

# FIGURE 78

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA161005
><subunit 1 of 1, 802 aa, 1 stop
><MW: 92235, pI: 6.80, NX(S/T): 5
MITLTELKCLADAQSSYHILKPWWDVFWYYITLIMLLVAVLAGALQLTQSRVLCCLPCKV
EFDNHCAVPWDILKASMNTSSNPGTPLPLPLRIQNDLHRQQYSYIDAVCYEKQLHWFAKF
FPYLVLLHTLIFAACSNFWLHYPSTSSRLEHFVAILHKCFDSPWTTRALSETVAEQSVRP
LKLSKSKILLSSSGCSADIDSGKQSLPYPQPGLESAGIESPTSSGLDKKEGEQAKAIFEK
VKRFRMHVEQKDIIYRVYLKQIIVKVILFVLIITYVPYFLTHITLEIDCSVDVQAFTGYK
RYQCVYSLAEIFKVLASFYVILVILYGLTSSYSLWWMLRSSLKQYSFEALREKSNYSDIP
DVKNDFAFILHLADQYDPLYSKRFSIFLSEVSENKLKQINLNNEWTVEKLKSKLVKNAQD
KIELHLFMLNGLPDNVFELTEMEVLSLELIPEVKLPSAVSQLVNLKELRVYHSSLVVDHP
ALAFLEENLKILRLKFTEMGKIPRWVFHLKNLKELYLSGCVLPEQLSTMQLEGFQDLKNL
RTLYLKSSLSRIPQVVTDLLPSLQKLSLDNEGSKLVVLNNLKKMVNLKSLELISCDLERI
PHSIFSLNNLHELDLRENNLKTVEEISFQHLQNLSCLKLWHNNIAYIPAQIGALSNLEQL
SLDHNNIENLPLQLFLCTKLHYLDLSYNHLTFIPEEIQYLSNLQYFAVTNNNIEMLPDGL
FQCKKLQCLLLGKNSLMNLSPHVGELSNLTHLELIGNYLETLPPELEGCQSLKRNCLIVE
ENLLNTLPLPVTERLQTCLDKC

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-46

**Transmembrane domains:**
Amino acids 118-138;261-281;311-332

**N-glycosylation sites:**
Amino acids 78-82;355-359;633-637;748-752

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 382-386

**Tyrosine kinase phosphorylation site:**
Amino acids 21-30

**N-myristoylation sites:**
Amino acids 212-218;327-333;431-437;652-658;
719-725

**Prokaryotic membrane lipoprotein lipid attachment site:**
Amino acids 125-136

**Leucine zipper pattern:**
Amino acids 468-490

**Leucine Rich Repeat:**
Amino acids 609-632; 748-770

# FIGURE 79

CGGACGCGTGGGCCGCGCTCCCTCACGGCCCCTCGGCGGCGCCCGTCGGATCCGGCCTCTCT
CTGCGCCCCGGGGCGCGCCACCTCCCCGCCGGAGGTGTCCACGCGTCCGGCCGTCCATCCGT
CCGTCCCTCCTGGGGCCGGCGCTGACC**ATG**CCCAGCGGCTGCCGCTGCCTGCATCTCGTGTG
CCTGTTGTGCATTCTGGGGGCTCCCGGTCAGCCTGTCCGAGCCGATGACTGCAGCTCCCACT
GTGACCTGGCCCACGGCTGCTGTGCACCTGACGGCTCCTGCAGGTGTGACCCGGGCTGGGAG
GGGCTGCACTGTGAGCGCTGTGTGAGGATGCCTGGCTGCCAGCACGGTACCTGCCACCAGCC
ATGGCAGTGCATCTGCCACAGTGGCTGGGCAGGCAAGTTCTGTGACAAAGATGAACATATCT
GTACCACGCAGTCCCCCTGCCAGAATGGAGGCCAGTGCATGTATGACGGGGGCGGTGAGTAC
CATTGTGTGTGCTTACCAGGCTTCCATGGGCGTGACTGCGAGCGCAAGGCTGGACCCTGTGA
ACAGGCAGGCTCCCCATGCCGCAATGGCGGGCAGTGCCAGGACGACCAGGGCTTTGCTCTCA
ACTTCACGTGCCGCTGCTTGGTGGGCTTTGTGGGTGCCCGCTGTGAGGTAAATGTGGATGAC
TGCCTGATGCGGCCTTGTGCTAACGGTGCCACCTGCCTTGACGGCATAAACCGCTTCTCCTG
CCTCTGTCCTGAGGGCTTTGCTGGACGCTTCTGCACCATCAACCTGGATGACTGTGCCAGCC
GCCCATGCCAGAGAGGGGCCCGCTGTCGGGACCGTGTCCACGACTTCGACTGCCTCTGCCCC
AGTGGCTATGGTGGCAAGACCTGTGAGCTTGTCTTACCTGTCCCAGACCCCCCAACCACAGTG
GACACCCCTCTAGGGCCCACCTCAGCTGTAGTGGTACCTGCTACGGGGCCAGCCCCCCACAG
CGCAGGGGCTGGTCTGCTGCGGATCTCAGTGAAGGAGGTGGTGCGGAGGCAAGAGGCTGGGC
TAGGTGAGCCTAGCTTGGTGGCCCTGGTGGTGTTTGGGGCCCTCACTGCTGCCCTGGTTCTG
GCTACTGTGTTGCTGACCCTGAGGGCCTGGCGCCGGGGTGTCTGCCCCCCTGGACCCTGTTG
CTACCCTGCCCCACACTATGCTCCAGCGTGCCAGGACCAGGAGTGTCAGGTTAGCATGCTGC
CAGCAGGGCTCCCCCTGCCACGTGACTTGCCCCCTGAGCCTGGAAAGACCACAGCACTG**TGA**
TGGAGGTGGGGGCTTTCTGGCCCCCTTCCTCACCTCTTCCACCCCTCAGACTGGAGTGGTCC
GTTCTCACCACCCTTCAGCTTGGGTACACACACAGAGGAGACCTCAGCCTCACACCAGAAAT
ATTATTTTTTTAATACACAGAATGTAAGATGGAATTTTATCAAATAAAACTATGAAAATGCA
AAAAAAAAAAAAAAA

# FIGURE 80

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA170245
><subunit 1 of 1, 383 aa, 1 stop
><MW: 40548, pI: 6.48, NX(S/T): 1
MPSGCRCLHLVCLLCILGAPGQPVRADDCSSHCDLAHGCCAPDGSCRCDPGWEGLHCERC
VRMPGCQHGTCHQPWQCICHSGWAGKFCDKDEHICTTQSPCQNGGQCMYDGGGEYHCVCL
PGFHGRDCERKAGPCEQAGSPCRNGGQCQDDQGFALNFTCRCLVGFVGARCEVNVDDCLM
RPCANGATCLDGINRFSCLCPEGFAGRFCTINLDDCASRPCQRGARCRDRVHDFDCLCPS
GYGGKTCELVLPVPDPPTTVDTPLGPTSAVVVPATGPAPHSAGAGLLRISVKEVVRRQEA
GLGEPSLVALVVFGALTAALVLATVLLTLRAWRRGVCPPGPCCYPAPHYAPACQDQECQV
SMLPAGLPLPRDLPPEPGKTTAL

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-21

**Transmembrane domain:**
Amino acids 306-331

**N-glycosylation site:**
Amino acids 157-160

**Glycosaminoglycan attachment site:**
Amino acids 240-243

**N-myristoylation sites:**
Amino acids 44-49;65-70;243-248;314-319

**Aspartic acid and asparagine hydroxylation sites:**
Amino acids 189-200;227-238

**EGF-like domain cysteine pattern signature:**
Amino acids 46-57;77-88;117-128;160-171;198-209;
236-247

**Zinc finger, C3HC4 type, signature:**
Amino acids 7-16

**EGF-like domain proteins:**
Amino acids 46-58;77-89;117-129;160-172;198-210;
216-228;236-248

# FIGURE 81

GTTTGTTGCTCAAACCGAGTTCTGGAGAACGCCATCAGCTCGCTGCTTAAAATTAAACCACA
GGTTCCATTATGGGTCGACTTGATGGGAAAGTCATCATCCTGACGGCCGCTGCTCAGGGGAT
TGGCCAAGCAGCTGCCTTAGCTTTTGCAAGAGAAGGTGCCAAAGTCATAGCCACAGACATTA
ATGAGTCCAAACTTCAGGAACTGGAAAAGTACCCGGGTATTCAAACTCGTGTCCTTGATGTC
ACAAAGAAGAAACAAATTGATCAGTTTGCCAGTGAAGTTGAGAGACTTGATGTTCTCTTTAAT
GTTGCTGGTTTTGTCCATCATGGAACTGTCCTGGATTGTGAGGAGAAAGACTGGGACTTCTC
GATGAATCTCAATGTGCGCAGCATGTACCTGATGATCAAGGCATTCCTTCCTAAAATGCTTG
CTCAGAAATCTGGCAATATTATCAACATGTCTTCTGTGGCTTCCAGCGTCAAAGGAGTTGTG
AACAGATGTGTGTACAGCACAACCAAGGCAGCCGTGATTGGCCTCACAAAATCTCTGGCTGC
AGATTTCATCCAGCAGGGCATCAGGTGCAACTGTGTGTGCCCAGGAACAGTTGATACGCCAT
CTCTACAAGAAAGAATACAAGCCAGAGGAAATCCTGAAGAGGCACGGAATGATTTCCTGAAG
AGACAAAAGACGGGAAGATTCGCAACTGCAGAAGAAATAGCCATGCTCTGCGTGTATTTGGC
TTCTGATGAATCTGCTTATGTAACTGGTAACCCTGTCATCATTGATGGAGGCTGGAGCTTGT
GATTTTAGGATCTCCATGGTGGGAAGGAAGGCAGGCCCTTCCTATCCACAGTGAACCTGGTT
ACGAAGAAAACTCACCAATCATCTCCTTCCTGTTAATCACATGTTAATGAAAATAAGCTCTT
TTTAATGATGTCACTGTTTGCAAGAGTCTGATTCTTTAAGTATATTAATCTCTTTGTAATCT
CTTCTGAAATCATTGTAAAGAAATAAAAATATTGAACTCAT

# FIGURE 82

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA171771
><subunit 1 of 1, 245 aa, 1 stop
><MW: 26711, pI: 8.00, NX(S/T): 2
MGRLDGKVIILTAAAQGIGQAAALAFAREGAKVIATDINESKLQELEKYPGIQTRVLDVT
KKKQIDQFASEVERLDVLFNVAGFVHHGTVLDCEEKDWDFSMNLNVRSMYLMIKAFLPKM
LAQKSGNIINMSSVASSVKGVVNRCVYSTTKAAVIGLTKSLAADFIQQGIRCNCVCPGTV
DTPSLQERIQARGNPEEARNDFLKRQKTGRFATAEEIAMLCVYLASDESAYVTGNPVIID
GGWSL

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-20

**N-glycosylation sites:**
Amino acids 39-43;130-134

**Tyrosine kinase phosphorylation site:**
Amino acids 42-50

**N-myristoylation sites:**
Amino acids 17-23;19-25;126-132;156-162;169-175

**Short-chain dehydrogenases/reductases family proteins:**
Amino acids 7-19;73-83;127-164; 169-178

**Short chain dehydrogenase:**
Amino acids 7-183

# FIGURE 83

GGGCGGCGGCGGCAGCGGTTGGAGGTTGTAGGACCGGCGAGGAATAGGAATCATGGCGGCTG
CGCTGTTCGTGCTGCTGGGATTCGCGCTGCTGGGCACCCACGGAGCCTCCGGGGCTGCCGGC
TTCGTCCAGGCGCCGCTGTCCCAGCAGAGGTGGGTGGGGGGCAGTGTGGAGCTGCACTGCGA
GGCCGTGGGCAGCCCGGTGCCCGAGATCCAGTGGTGGTTTGAAGGGCAGGGTCCCAACGACA
CCTGCTCCCAGCTCTGGGACGGCGCCCGGCTGGACCGCGTCCACATCCACGCCACCTACCAC
CAGCACGCGGCCAGCACCATCTCCATCGACACGCTCGTGGAGGAGGACACGGGCACTTACGA
GTGCCGGGCCAGCAACGACCCGGATCGCAACCACCTGACCCGGGCGCCCAGGGTCAAGTGGG
TCCGCGCCCAGGCAGTCGTGCTAGTCCTGGAACCCGGCACAGTCTTCACTACCGTAGAAGAC
CTTGGCTCCAAGATACTCCTCACCTGCTCCTTGAATGACAGCGCCACAGAGGTCACAGGGCA
CCGCTGGCTGAAGGGGGGCGTGGTGCTGAAGGAGGACGCGCTGCCCGGCCAGAAAACGGAGT
TCAAGGTGGACTCCGACGACCAGTGGGGAGAGTACTCCTGCGTCTTCCTCCCCGAGCCCATG
GGCACGGCCAACATCCAGCTCCACGGGCCTCCCAGAGTGAAGGCTGTGAAGTCGTCAGAACA
CATCAACGAGGGGGAGACGGCCATGCTGGTCTGCAAGTCAGAGTCCGTGCCACCTGTCACTG
ACTGGGCCTGGTACAAGATCACTGACTCTGAGGACAAGGCCCTCATGAACGGCTCCGAGAGC
AGGTTCTTCGTGAGTTCCTCGCAGGGCCGGTCAGAGCTACACATTGAGAACCTGAACATGGA
GGCCGACCCCGGCCAGTACCGGTGCAACGGCACCAGCTCCAAGGGCTCCGACCAGGCCATCA
TCACGCTCCGCGTGCGCAGCCACCTGGCCGCCCTCTGGCCCTTCCTGGGCATCGTGGCTGAG
GTGCTGGTGCTGGTCACCATCATCTTCATCTACGAGAAGCGCCGGAAGCCCGAGGACGTCCT
GGATGATGACGACGCCGGCTCTGCACCCCTGAAGAGCAGCGGGCAGCACCAGAATGACAAAG
GCAAGAACGTCCGCCAGAGGAACTCTTCCTGAGGCAGGTGGCCCGAGGACGCTCCCTGCTCC
ACGTCTGCGCCGCCGCCGGAGTCCACTCCCAGTGCTTGCAAGATTCCAAGTTCTCACCTCTT
AAAGAAAACCCACCCCGTAGATTCCCATCATACACTTCCTTCTTTTTTAAAAAAGTTGGGTT
TTCTCCATTCAGGATTCTGTTCCTTAGGTTTTTTTCCTTCTGAAGTGTTTCACGAGAGCCCG
GGAGCTGCTGCCCTGCGGCCCCGTCTGTGGCTTTCAGCCTCTGGGTCTGAGTCATGGCCGGG
TGGGCGGCACAGCCTTCTCCACTGGCCGGAGTCAGTGCCAGGTCCTTGCCCTTTGTGGAAAGTC
ACAGGTCACACGAGGGGCCCCGTGTCCTGCCTGTCTGAAGCCAATGCTGTCTGGTTGCGCCA
TTTTTGTGCTTTTATGTTTAATTTTATGAGGGCCACGGGTCTGTGTTCGACTCAGCCTCAGG
GACGACTCTGACCTCTTGGCCACAGAGGACTCACTTGCCCACACCGAGGGCGACCCCGTCAC
AGCCTCAAGTCACTCCCAAGCCCCCTCCTTGTCTGTGCATCCGGGGGCAGCTCTGGAGGGGG
TTTGCTGGGGAACTGGCGCCATCGCCGGGACTCCAGAACCGCAGAAGCCTCCCCAGCTCACC
CCTGGAGGACGGCCGGCTCTCTATAGCACCAGGGCTCACGTGGGAACCCCCCTCCCACCCAC
CGCCACAATAAAGATCGCCCCCACCTCCACCCAAAAA

# FIGURE 84

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA173157
><subunit 1 of 1, 385 aa, 1 stop
><MW: 42200, pI: 5.57, NX(S/T): 5
MAAALFVLLGFALLGTHGASGAAGFVQAPLSQQRWVGGSVELHCEAVGSPVPEIQWWFEG
QGPNDTCSQLWDGARLDRVHIHATYHQHAASTISIDTLVEEDTGTYECRASNDPDRNHLT
RAPRVKWVRAQAVVLVLEPGTVFTTVEDLGSKILLTCSLNDSATEVTGHRWLKGGVVLKE
DALPGQKTEFKVDSDDQWGEYSCVFLPEPMGTANIQLHGPPRVKAVKSSEHINEGETAML
VCKSESVPPVTDWAWYKITDSEDKALMNGSESRFFVSSSQGRSELHIENLNMEADPGQYR
CNGTSSKGSDQAIITLRVRSHLAALWPFLGIVAEVLVLVTIIFIYEKRRKPEDVLDDDDA
GSAPLKSSGQHQNDKGKNVRQRNSS

**Important features of the protein:**

| | |
|---|---|
| **Signal peptide:** | |
| Amino acids | 1-18 |
| **Transmembrane domain:** | |
| Amino acids | 320-343 |
| **N-glycosylation sites:** | |
| Amino acids | 64-68;160-164;268-272;302-306 |
| **N-myristoylation sites:** | |
| Amino acids | 15-21;18-24;60-66;104-110;140-146; 297-303;308-314;369-375 |
| **Immunoglobulin domain:** | |
| Amino acids | 37-110;150-205;235-303 |

# FIGURE 85

GGCTCGAGCAAAGACATACGAACAGGGAGGAAGGCCGACTGAAAGAAAGACGGAGAAGAGGA
GAGAGAAGCCAGGGCCGAGCGTGCCAGCAGGCGGATGGAGGGCGGCCTGGTGGAGGAGGAGA
CGTAGTGGCCTGGGCTGAGCTGGGTGGGCCGGGAGAAGCGGGTGCCTCAGAGTGGGGGTGGG
GGC**ATG**GGAGGGGCAGGCATTCTGCTGCTGCTGCTGGCTGGGGCGGGGGTGGTGGTGGCCTGG
AGACCCCCAAAGGGAAAGTGTCCCCTGCGCTGCTCCTGCTCTAAAGACAGCGCCCTGTGTGA
GGGCTCCCCGGACCTGCCCGTCAGCTTCTCTCCGACCCTGCTGTCACTCTCACTCGTCAGGA
CGGGAGTCACCCAGCTGAAGGCCGGCAGCTTCCTGAGAATTCCGTCTCTGCACCTGCTCCTC
TTCACCTCCAACTCCTTCTCCGTGATTGAGGACGATGCATTTGCGGGCCTGTCCCACCTGCA
GTACCTCTTCATCGAGGACAATGAGATTGGCTCCATCTCTAAGAATGCCCTCAGAGGACTTC
GCTCGCTTACACACCTAAGCCTGGCCAATAACCATCTGGAGACCCTCCCCAGATTCCTGTTC
CGAGGCCTGGACACCCTTACTCACGTGGACCTCCGCGGGAACCCGTTCCAGTGTGACTGCCG
CGTCCTCTGGCTCCTGCAGTGGATGCCCACCGTGAATGCCAGCGTGGGGACCGGCGCCTGTG
CGGGCCCCGCCTCCCTGAGCCACATGCAGCTCCACCACCTCGACCCCAAGACTTTCAAGTGC
AGAGCCATAGGTGGGGGGCTTTCCCGATGGGGTGGGAGGCGGGAGATCTGGGGGAAAGGCTG
CCAGGGCCAAGAGGCTCGTCTCACTCCCTGCCCTGCCATTTCCCGGAGTGGGAAGACCCTGA
GCAAGCAGCACTGCCTTCCTGAGCCCCAGTTTTCTCATCTG**TAA**AGTGGGGGTAATAAACAG
TGATATAGG

# FIGURE 86

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA175734
><subunit 1 of 1, 261 aa, 1 stop
><MW: 28231, pI: 9.28, NX(S/T): 1
MGGAGILLLLLAGAGVVVAWRPPKGKCPLRCSCSKDSALCEGSPDLPVSFSPTLLSLSLV
RTGVTQLKAGSFLRIPSLHLLLFTSNSFSVIEDDAFAGLSHLQYLFIEDNEIGSISKNAL
RGLRSLTHLSLANNHLETLPRFLFRGLDTLTHVDLRGNPFQCDCRVLWLLQWMPTVNASV
GTGACAGPASLSHMQLHHLDPKTFKCRAIGGGLSRWGGRREIWGKGCQGQEARLTPCPAI
SRSGKTLSKQHCLPEPQFSHL

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-19

**N-glycosylation site:**
Amino acids 177-181

**N-myristoylation sites:**
Amino acids 15-21;181-186;210-215

**Amidation site:**
Amino acids 217-220

**Microbodies C-terminal targeting signal:**
Amino acids 259-262

**ATP/GTP-binding site motif A (P-loop):**
Amino acids 239-246

**Leucine zipper pattern:**
Amino acids 129-150

**Leucine Rich Repeat:**
Amino acids 53-76; 149-171

**Leucine rich repeat C-terminal domain:**
Amino acids 158-207

# FIGURE 87

CGGACGCGTGGGGCGGCGAGAGCAGCTGCAGTTCGCATCTCAGGCAGTACCTAGAGGAGCTG
CCGGTGCCTCCTCAGAACATCTCCTGATCGCTACCCAGGACCAGGCACCAAGGACAGGGAGT
CCCAGGCGCACACCCCCCATTCTGGGTCCCCCAGGCCCAGACCCCCACTCTGCCACAGGTTG
CATCTTGACCTGGTCCTCCTGCAGAAGTGGCCCCTGTGGTCCTGCTCTGAGACTCGTCCCTG
GGCGCCCCTGCAGCCCCTTTCTATGACTCCATCTGGATTTGGCTGGCTGTGGGGACGCGGTC
CGAGGGGCGGCCTGGCTCTCAGCGTGGTGGCAGCCAGCTCTCTGGCCACCATGGCAAATGCT
GAGATCTGAGGGGACAAGGCTCTACAGCCTCAGCCAGGGGCACTCAGCTGTTGCAGGGTGTG
**ATG**GAGAACAAAGCTATGTACCTACACACCGTCAGCGACTGTGACACCAGCTCCATCTGTGA
GGATTCCTTTGATGGCAGGAGCCTGTCCAAGCTGAACCTGTGTGAGGATGGTCCATGTCACA
AACGGCGGGCAAGCATCTGCTGTACCCAGCTGGGGTCCCTGTCGGCCCTGAAGCATGCTGTC
CTGGGGCTCTACCTGCTGGTCTTCCTGATTCTTGTGGGCATCTTCATCTTAGCAGGGCCACC
GGGACCCAAAGGTGATCAGGGGGATGAAGGAAAGGAAGGCAGGCCTGGCATCCCTGGATTGC
CTGGACTTCGAGGTCTGCCCGGGGAGAGAGGTACCCCAGGATTGCCCGGGCCCAAGGGCGAT
GATGGGAAGCTGGGGGCCACAGGACCAATGGGCATGCGTGGGTTCAAAGGTGACCGAGGCCC
AAAAGGAGAGAAAGGAGAGAAAGGAGACAGAGCTGGGGATGCCAGTGGCGTGGAGGCCCCGA
TGATGATCCGCCTGGTGAATGGCTCAGGTCCGCACGAGGGCCGCGTGGAAGTGTACCACGAC
CGGCGCTGGGGCACCGTGTGTGACGACGGCTGGGACAAGAAGGACGGAGACGTGGTGTGCCG
CATGCTCGGCTTCCGCGGTGTGGAGGAGGTGTACCGCACAGCTCGATTCGGGCAAGGCACTG
GGAGGATCTGGATGGATGACGTTGCCTGCAAGGGCACAGAGGAAACCATCTTCCGCTGCAGC
TTCTCCAAATGGGGGGTGACAAACTGTGGACATGCCGAAGATGCCAGCGTGACATGCAACAG
ACAC**TGA**AAGTGGGCAGAGCCCAAGTTCGGGGTCCTGCACAGAGCACCCTTGCTGCATCCCT
GGGGTGGGGCACAGCTCGGGGCCACCCTGACCATGCCTCGACCACACCCCGTCCAGCATTCT
CAGTCCTCACACCTGCATCCCAGGACCGTGGGGGCCGGTCGTCATTTCCCTCTTGAACATGT
GCTCCGAAGTATAACTCTGGGACCTACTGCCCGTCTCTCTCTTCCACCAGGTTCCTGCATGA
GGAGCCCTGATCAACTGGATCACCACTTTGCCCAGCCTCTGAACACCATGCACCAGGCCTCA
ATATCCCAGTTCCCTTTGGCCTTTTAGTTACAGGTGAATGCTGAGAATGTGTCAGAGACAAG
TGCAGCAGCAGCGATGGTTGGTAGTATAGATCATTTACTCTTCAGACAATTCCCAAACCTCC
ATTAGTCCAAGAGTTTCTACATCTTCCTCCCCAGCAAGAGGCAACGTCAAGTGATGAATTTC
CCCCCTTTACTCTGCCTCTGCTCCCCATTTGCTAGTTTGAGGAAGTGACATAGAGGAGAAGC
CAGCTGTAGGGGCAAGAGGGAAATGCAAGTCACCTGCAGGAATCCAGCTAGATTTGGAGAAG
GGAATGAAACTAACATTGAATGACTACCATGGCACGCTAAATAGTATCTTGGGTGCCAAATTCA
TGTATCCACTTAGCTGCATTGGTCCAGGGCATGTCAGTCTGGATACAGCCTTACCTTCAGGT
AGCACTTAACTGGTCCATTCACCTAGACTGCAAGTAAGAAGACAAAATGACTGAGACCGTGT
GCCCACCTGAACTTATTGTCTTTACTTGGCCTGAGCTAAAAGCTTGGGTGCAGGACCTGTGT
AACTAGAAAGTTGCCTACTTCAGAACCTCCAGGGCGTGAGTGCAAGGTCAAACATGACTGGC
TTCCAGGCCGACCATCAATGTAGGAGGAGAGCTGATGTGGAGGGTGACATGGGGGCTGCCCA
TGTTAAACCTGAGTCCAGTGCTCTGGCATTGGGCAGTCACGGTTAAAGCCAAGTCATGTGTG
TCTCAGCTGTTTGGAGGTGATGATTTTGCATCTTCCAAGCCTCTTCAGGTGTGAATCTGTGG
TCAGGAAAACACAAGTCCTAATGGAACCCTTAGGGGGGAAGGAAATGAAGATTCCCTATAAC
CTCTGGGGGTGGGGAGTAGGAATAAGGGGCCTTGGGCCTCCATAAATCTGCAATCTGCACCC
TCCTCCTAGAGACAGGGAGATCGTGTTCTGCTTTTTACATGAGGAGCAGAACTGGGCCATAC
ACGTGTTCAAGAACTAGGGGAGCTACCTGGTAGCAAGTGAGTGCAGACCCACCTCACCTTGG
GGGAATCTCAAACTCATAGGCCTCAGATACACGATCACCTGTCATATCAGGTGAGCACTGGC
CTGCTTGGGGAGAGACCTGGGCCCCTCCAGGTGTAGGAACAGCAACACTCCTGGCTGACAAC
TAAGCCAATATGGCCCTAGGTCATTCTTGCTTCCAATATGCTTGCCACTCCTTAAATGTCCT
AATGATGAGAAACTCTCTTTCTGACCAATTGCTATGTTTACATAACACGCATGTACTCATGC
ATCCCTTGCCAGAGCCCATATATGTATGCATATATAAACATAGCACTTTTTACTACATAGCT
CAGCACATTGCAAGGTTTGCATTTAAGTT

# FIGURE 88

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA176108
><subunit 1 of 1, 270 aa, 1 stop
><MW: 28871, pI: 7.09, NX(S/T): 1
MENKAMYLHTVSDCDTSSICEDSFDGRSLSKLNLCEDGPCHKRRASICCTQLGSLSALKH
AVLGLYLLVFLILVGIFILAGPPGPKGDQGDEGKEGRPGIPGLPGLRGLPGERGTPGLPG
PKGDDGKLGATGPMGMRGFKGDRGPKGEKGEKGDRAGDASGVEAPMMIRLVNGSGPHEGR
VEVYHDRRWGTVCDDGWDKKDGDVVCRMLGFRGVEEVYRTARFGQGTGRIWMDDVACKGT
EETIFRCSFSKWGVTNCGHAEDASVTCNRH

**Transmembrane domain:**
Amino acids 55-80

**N-glycosylation site:**
Amino acids 172-175

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 43-46

**Tyrosine kinase phosphorylation site:**
Amino acids 212-218

**N-myristoylation sites:**
Amino acids 53-58;224-229;239-244;253-258

**Speract receptor repeated domain signature:**
Amino acids 173-211

**Scavenger receptor cysteine-rich domain:**
Amino acids 171-268

**Collagen Collagen triple helix repeat:**
Amino acids 90-149

# FIGURE 89

GTCGCCGCGAGGGACGCAGAGAGCACCCTCCACGCCCAGATGCCTGCGTAGTTTTTGTGACC
AGTCCGCTCCTGCCTCCCCCTGGGGCAGTAGAGGGGGAGCG**ATG**GAGAACTGGACTGGCAGG
CCCTGGCTGTATCTGCTGCTGCTTCTGTCCCTCCCTCAGCTCTGCTTGGATCAGGAGGTGTT
GTCCGGACACTCTCTTCAGACACCTACAGAGGAGGGCCAGGGCCCCGAAGGTGTCTGGGGAC
CTTGGGTCCAGTGGGCCTCTTGCTCCCAGCCCTGCGGGGTGGGGGTGCAGCGCAGGAGCCGG
ACATGTCAGCTCCCTACAGTGCAGCTCCACCCGAGTCTGCCCCTCCCTCCCCGGCCCCCAAG
ACATCCAGAAGCCCTCCTCCCCCGGGGCCAGGGTCCCAGACCCCAGACTTCTCCAGAAACCC
TCCCCTTGTACAGGACACAGTCTCGGGGAAGGGGTGGCCCACTTCGAGGTCCCGCTTCCCAC
CTAGGGAGAGAGGAGACCCAGGAGATTCGAGCGGCCAGGAGGTCCCGGCTTCGAGACCCCAT
CAAGCCAGGAATGTTCGGTTATGGGAGAGTGCCCTTTGCATTGCCACTGCACCGGAACCGCA
GGCACCCTCGGAGCCCACCCAGATCTGAGCTGTCCCTGATCTCTTCTAGAGGGGAAGAGGCT
ATTCCGTCCCCTACTCCAAGAGCAGAGCCATTCTCCGCAAACGGCAGCCCCCAAACTGAGCT
CCCTCCCACAGAACTGTCTGTCCACACCCCATCCCCCCAAGCAGAACCTCTAAGCCCTGAAA
CTGCTCAGACAGAGGTGGCCCCCAGAACCAGGCCTGCCCCCCTACGGCATCACCCCAGAGCC
CAGGCCTCTGGCACAGAGCCCCCCTCACCCACGCACTCCTTAGGAGAAGGTGGCTTCTTCCG
TGCATCCCCTCAGCCACGAAGGCCAAGTTCCCAGGGTTGGGCCAGTCCCCAGGTAGCAGGGA
GACGCCCTGATCCTTTTCCTTCGGTCCCTCGGGGCCGAGGCCAGCAGGGCCAAGGGCCTTGG
GGAACGGGGGGGACTCCTCACGGGCCCCGCCTGGAGCCTGACCCTCAGCACCCGGGCGCCTG
GCTGCCCCTGCTGAGCAACGGCCCCCATGCCAGCTCCCTCTGGAGCCTCTTTGCTCCCAGTA
GCCCTATTCCAAGATGTTCTGGGGAGAGTGAACAGCTAAGAGCCTGCAGCCAAGCGCCCTGC
CCCCCTGAGCAGCCAGACCCCCGGGCCCTGCAGTGCGCAGCCTTTAACTCCCAGGAATTCATG
GGCCAGCTGTATCAGTGGGAGCCCTTCACTGAAGTCCAGGGCTCCCAGCGCTGTGAACTGAA
CTGCCGGCCCCGTGGCTTCCGCTTCTATGTCCGTCACACTGAAAAGGTCCAGGATGGGACCC
TGTGTCAGCCTGGAGCCCCTGACATCTGTGTGGCTGGACGCTGTCTGAGCCCCGGCTGTGAT
GGGATCCTTGGCTCTGGCAGGCGTCCTGATGGCTGTGGAGTCTGTGGGGGTGATGATTCTAC
CTGTCGCCTTGTTTCGGGGAACCTCACTGACCGAGGGGGCCCCCTGGGCTATCAGAAGATCT
TGTGGATTCCAGCGGGAGCCTTGCGGCTCCAGATTGCCCAGCTCCGGCCTAGCTCCAACTAC
CTGGCACTTCGTGGCCCTGGGGGCCGGTCCATCATCAATGGGAACTGGGCTGTGGATCCCCC
TGGGTCCTACAGGGCCGGCGGGACCGTCTTTCGATATAACCGTCCTCCCAGGGAGGAGGGCA
AAGGGGAGAGTCTGTCGGCTGAAGGCCCCACCACCCAGCCTGTGGATGTCTATATGATCTTT
CAGGAGGAAAACCCAGGCGTTTTTTATCAGTATGTCATCTCTTCACCTCCTCCAATCCTTGA
GAACCCCACCCCAGAGCCCCCTGTCCCCCAGCTTCAGCCGGAGATTCTGAGGGTGGAGCCCC
CACTTGCTCCGGCACCCCGCCCAGCCCGGACCCCAGGCACCCTCCAGCGTCAGGTGCGGATC
CCCCAGATGCCCGCCCCGCCCCATCCCAGGACACCCCTGGGGGTCTCCAGCTGCGTACTGGAA
ACGAGTGGGACACTCTGCATGCTCAGCGTCCTGCGGGAAAGGTGTCTGGCGCCCCATTTTCC
TCTGCATCTCCCGTGAGTCGGGAGAGGAACTGGATGAACGCAGCTGTGCCGCGGGTGCCAGG
CCCCCAGCCTCCCCTGAACCCTGCCACGGCACCCCATGCCCCCCATACTGGGAGGCTGGCGA
GTGGACATCCTGCAGCCGCTCCTGTGGCCCCGGCACCCAGCACCGCCAGCTGCAGTGCCGGC
AGGAATTTGGGGGGGGTGGCTCCTCGGTGCCCCCGGAGCGCTGTGGACATCTCCCCCGGCCC
AACATCACCCAGTCTTGCCAGCTGCGCCTCTGTGGCCATTGGGAAGTTGGCTCTCCTTGGAG
CCAGTGCTCCGTGCGGTGCGGCCGGGGCCAGAGAAGCCGGCAGGTTCGCTGTGTTGGGAACA
ACGGTGATGAAGTGAGCGAGCAGGAGTGTGCGTCAGGCCCCCCACAGCCCCCCAGCAGAGAG
GCCTGTGACATGGGGCCCTGTACTACTGCCTGGTTCCACAGCGACTGGAGCTCCAAGGTGAG
CCCGGAACCCCCAGCCATATCCTGCATCCTGGGTAACCATGCCCAGGACACCTCAGCCTTTC
CAGCA**TAG**CTCAATAAACTTGTATTGATC

# FIGURE 90

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA190710
><subunit 1 of 1, 877 aa, 1 stop
><MW: 95132, pI: 8.77, NX(S/T): 5

MENWTGRPWLYLLLLLSLPQLCLDQEVLSGHSLQTPTEEGQGPEGVWGPWVQWASCSQPC
GVGVQRRSRTCQLPTVQLHPSLPLPPRPPRHPEALLPRGQGPRPQTSPETLPLYRTQSRG
RGGPLRGPASHLGREETQEIRAARRSRLRDPIKPGMFGYGRVPFALPLHRNRRHPRSPPR
SELSLISSRGEEAIPSPTPRAEPFSANGSPQTELPPTELSVHTPSPQAEPLSPETAQTEV
APRTRPAPLRHHPRAQASGTEPPSPTHSLGEGGFFRASPQPRRPSSQGWASPQVAGRRPD
PFPSVPRGRGQQGQGPWGTGGTPHGPRLEPDPQHPGAWLPLLSNGPHASSLWSLFAPSSP
IPRCSGESEQLRACSQAPCPPEQPDPRALQCAAFNSQEFMGQLYQWEPFTEVQGSQRCEL
NCRPRGFRFYVRHTEKVQDGTLCQPGAPDICVAGRCLSPGCDGILGSGRRPDGCGVCGGD
DSTCRLVSGNLTDRGGPLGYQKILWIPAGALRLQIAQLRPSSNYLALRGPGGRSIINGNW
AVDPPGSYRAGGTVFRYNRPPREEGKGESLSAEGPTTQPVDVYMIFQEENPGVFYQYVIS
SPPPILENPTPEPPVPQLQPEILRVEPPLAPAPRPARTPGTLQRQVRIPQMPAPPHPRTP
LGSPAAYWKRVGHSACSASCGKGVWRPIFLCISRESGEELDERSCAAGARPPASPEPCHG
TPCPPYWEAGEWTSCSRSCGPGTQHRQLQCRQEFGGGGSSVPPERCGHLPRPNITQSCQL
RLCGHWEVGSPWSQCSVRCGRGQRSRQVRCVGNNGDEVSEQECASGPPQPPSREACDMGP
CTTAWFHSDWSSKVSPEPPAISCILGNHAQDTSAFPA

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-24

**N-glycosylation sites:**
Amino acids 3-6;490-493;773-776

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 282-285

**N-myristoylation sites:**
Amino acids 208-213;414-419;463-468;473-478;475-480;
478-483;495-500;546-551;662-667;755-760;
756-761;789-794

**Amidation sites:**
Amino acids 295-298;467-470

**Leucine zipper pattern:**
Amino acids 504-526

**VWFC domain proteins:**
Amino acids 53-67;732-746;792-806

**Thrombospondin type 1 domain:**
Amino acids 48-87;727-783;787-841

# FIGURE 91

CGAGTATTTTCCCACCATCTCCAGCCGGAAACTGACCAAGAACTCTGAGGCGGATGGCATGT
TCGCGTACGTCTTCCATGATGAGTTCGTGGCCTCGATGATTAAGATCCCTTCGGACACCTTC
ACCATCATCCCTGACTTTGATATCTACTATGTCTATGGTTTTAGCAGTGGCAACTTTGTCTA
CTTTTTGACCCTCCAACCTGAGATGGTGTCTCCACCAGGCTCCACCACCAAGGAGCAGGTGT
ATACATCCAAGCTCGTGAGGCTTTGCAAGGAGGACACAGCCTTCAACTCCTATGTAGAGGTG
CCCATTGGCTGTGAGCGCAGTGGGGTGGAGTACCGCCTGCTGCAGGCTGCCTACCTGTCCAA
AGCGGGGGCCGTGCTTGGCAGGACCCTTGGAGTCCATCCAGATGATGACCTGCTCTTCACCG
TCTTCTCCAAGGGCCAGAAGCGGAAAATGAAATCCCTGGATGAGTCGGCCCTGTGCATCTTC
ATCTTGAAGCAGATAAATGACCGCATTAAGGAGCGGCTGCAGTCTTGTTACCGGGGCGAGGG
CACGCTGGACCTGGCCTGGCTCAAGGTGAAGGACATCCCCTGCAGCAGTGCGCTCTTAACCA
TTGACGATAACTTCTGTGGCCTGGACATGAATGCTCCCCTGGGAGTGTCCGACATGGTGCGT
GGAATTCCCGTCTTCACGGAGGACAGGGACCGCATGACGTCTGTCATCGCATATGTCTACAA
GAACCACTCTCTGGCCTTTGTGGGCACCAAAAGTGGCAAGCTGAAGAAGGTGCCTGGTACCA
GCCTCTGCCCTACCCTTGAGCTACAGACGGGACCCCGATCCCACAGAGCAACAGTGACTCTG
GAACTCCTGTTCTCCAGCTGTTCATCAAACTGAGAAAAACTTCAGAGCTGTGTAGGCTTATT
TAGTGTGTTGTCAGCCTTGGATATTGGAAAATGGAAACAGATGAGACACATCTACCTCCCTG
TGACCCCAGCCATACATCATAGCTCATGTCCTGCCACCCCAAGTCCTTAGGGAAAAAAGACT
TTGGAGAATGTGTCTCTGCTTAGCTTGGCTAGGTAGTTGGTCTCTTTTCTCTGCCCCAAGCG
TCCCCTGGGTAATTTTGGACAATGGAGTGTAGGCATGTTTGACTCTTGTGGTGTTATCACTT
GTATATGTCAGTGAAACTAACTGATTCTCCCATCGGAATATAGTTATCTCTTGGGCCTGATA
TATGGTAGGATAACCTTATGCTCATCTGTCCACTTCTGCAGCCAAGTCGCCTGGCCAGTGTG
TGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTATGCTTATCTGTGTTTAAAGGTGTGTG
TGCATACACAGGGCAGAGAGGATGGAGCCCACCGTACTGCAGCATCATGTAATTAACTCAGT
GCTCAGAACCATCCCAGCCTCTGCGGGAAAGAGAAAAGTAAGCCAACAGTGCCTGATGAGCT
GATCATATGTGCAAAAGCTCTGTTGGCATCTGGTCCAGGAGAGCACCCAAAAAAAGTTAATT
GGTGTTGTCCAGTCTCCTTTCCTTAAGACTATGGTTACAACAAAGCGTGAGCAGTGTCTCCT
GCATGGCCACTATCCAGCACAATTCCATAATTCCCCCATAGAGCCGGTGGGGAGGAGGAGGT
GAGTGGCGAAGGAAGTGGAAACACTTGGTGTCATGTGCTCCTATCATTTCTACTAGCTTACT
GGGAAATAAAGTGTAGTCAAGAGTGTATGAAGGCAAGATGTAAAATTAGCGACTGGTGCTAA
TCTGGTTACTTGAAAACAAGTGAAAGTGCTGTAGATTTGTTCTGTTGCTAAGAACCACCACA
CTAAACCTCGTATAGTTCCTGGAGGATATACAACAGTGTAATTCTCTTTAGGGTGTGCCACA
GGTTCCTGGCCTGTGGGAGGGAATGAATCAGGAGGGCTCTTGAGAACCTTCATCTGTGTGCT
TGCACTGAAAGTGAGTCCCAAAGCTGGAGATTTAGTGAGAGCAGGCAACCCCTCTGTGTCTC
ACTGTCCATATTCTGGAGGCAGAGGTTTGTAACAGGCCATGTGCACCTGCATAGGGATGGGT
AAAGCAAGGACTTTGAAAGAGTTGAAAAGCATTATAAACAGTTGTTCAGAAATACGTCCCAG
GAGTTCCATGTGAAACTGGCTCTGTGTGCATTGAAGCATGGCTGTTGGGAATTCTAACTGGT
CCAACACTCCTGCAAAACAATGTGTAAATATTTAGGAAGAAACTTGAAAATAGTCAAATCCT
TTGAACTGGTGACAATTTTTTAAAGAATCAATTCTAATTTGTTTCAAGGGTAATAATCACCA
AGATACACATTTCAGCATTTATTTAGTCTATCAAAAATTGGAATTGATATATACACTCATTT
ATAGGAGAATGGTTAGGTAGATTTGGTATATTTATGTAGTCATTGAAAACTTAGTTTATAAA
GGCCAATCTTGTAACTGATTCTTGTGTGATAACATTCAGTGAAAAAGCATGAGACAATTAGA
AAGCATGATACAATGAATAAAATAAAAACTGGAAAGAGAACCATCAAAATGCTAA

# FIGURE 92

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA190803
><subunit 1 of 1, 280 aa, 1 stop
><MW: 31222, pI: 7.40, NX(S/T): 1
MFAYVFHDEFVASMIKIPSDTFTIIPDFDIYYVYGFSSGNFVYFLTLQPEMVSPPGSTTK
EQVYTSKLVRLCKEDTAFNSYVEVPIGCERSGVEYRLLQAAYLSKAGAVLGRTLGVHPDD
DLLFTVFSKGQKRKMKSLDESALCIFILKQINDRIKERLQSCYRGEGTLDLAWLKVKDIP
CSSALLTIDDNFCGLDMNAPLGVSDMVRGIPVFTEDRDRMTSVIAYVYKNHSLAFVGTKS
GKLKKVPGTSLCPTLELQTGPRSHRATVTLELLFSSCSSN

**Important features of the protein:**

**N-glycosylation site:**
Amino acids 230-233

**N-myristoylation sites:**
Amino acids 87-92;107-112;194-199;237-242

# FIGURE 93

CCTTATCAGACAAAGGACGAGATGGAAAATACAAGATAATTTACAGTGGAGAAGAATTAGAA
TGTAACCTGAAAGATCTTAGACCAGCAACAGATTATCATGTGAGGGTGTATGCC**ATG**TACAA
TTCCGTAAAGGGATCCTGCTCCGAGCCTGTTAGCTTCACCACCCACAGCTGTGCACCCGAGT
GTCCTTTCCCCCCTAAGCTGGCACATAGGAGCAAAAGTTCACTAACCCTGCAGTGGAAGGCA
CCAATTGACAACGGTTCAAAAATCACCAACTACCTTTTAGAGTGGGATGAGGGAAAAAGAAA
TAGTGGTTTCAGACAGTGCTTCTTCGGGAGCCAGAAGCACTGCAAGTTGACAAAGCTTTGTC
CGGCAATGGGGTACACATTCAGGCTGGCCGCTCGAAACGACATTGGCACCAGTGGTTATAGC
CAAGAGGTGGTGTGCTACACATTAGGAAATATCCCTCAGATGCCTTCTGCACTAAGGCTGGT
TCGAGCTGGCATCACATGGGTCACGTTGCAGTGGAGTAAGCCAGAAGGCTGTTCACCCGAGG
AAGTGATCACCTACACCTTGGAAATTCAGGAGGATGAAAATGATAACCTTTTCCACCCAAAA
TACACTGGAGAGGATTTAACCTGTACTGTGAAAAATCTCAAAAGAAGCACACAGTATAAATT
CAGGCTGACTGCTTCTAATACGGAAGGAAAAAGCTGTCCAAGCGAAGTTCTTGTTTGTACGA
CGAGTCCTGACAGGCCTGGACCTCCTACCAGACCGCTTGTCAAAGGCCCAGTTACATCTCAT
GGCTTTAGTGTCAAATGGGATCCCCCTAAGGACAATGGTGGTTCAGAAATCCTCAAGTACTT
GCTAGAGATTACTGATGGAAATTCTGAAGCGAATCAGTGGGAAGTGGCCTACAGTGGGTCGG
CTACCGAATACACCTTCACCCACTTGAAACCAGGCACTTTGTACAAACTCCGAGCATGCTGC
ATCAGTACCGGCGGACACAGCCAGTGTTCTGAAAGTCTCCCTGTTCGCACACTAAGCATTGC
ACCAGGTCAATGTCGACCACCGAGGGTTTTGGGTAGACCAAAGCACAAAGAAGTCCACTTAG
AGTGGGATGTTCCTGCATCGGAAAGTGGCTGTGAGGTCTCAGAGTACAGCGTGGAGATGACG
GAGCCCGAAGACGTAGCCTCGGAAGTGTACCATGGCCCAGAGCTGGAGTGCACCGTCGGCAA
CCTGCTTCCTGGAACCGTGTATCGCTTCCGGGTGAGGGCTCTGAATGATGGAGGGTATGGTC
CCTATTCTGATGTCTCAGAAATTACCACTGCTGCAGGGCCTCCTGGACAATGCAAAGCACCT
TGTATTTCTTGTACACCTGATGGATGTGTCTTAGTGGGTTGGGAGAGTCCTGATAGTTCTGG
TGCTGACATCTCAGAGTACAGGTTGGAATGGGGAGAAGATGAAGAATCCTTAGAACTCATTT
ATCATGGGACAGACACCCGTTTTGAAATAAGAGACCTGTTGCCTGCTGCACAGTATTGCTGT
AGACTACAGGCCTTCAATCAAGCAGGGGCAGGGCCGTACAGTGAACTTGTCCTTTGCCAGAC
GCCAGCGTCTGCCCCTGACCCCGTCTCCACTCTCTGTGTCCTGGAGGAGGAGCCCCTTGATGCC
TACCCTGATTCACCTTCTGCGTGCCTTGTACTGAACTGGGAAGAGCCGTGCAATAACGGATC
TGAAATCCTTGCTTACACCATTGATCTAGGAGACACTAGCATTACCGTGGGCAACACCACCA
TGCATGTTATGAAAGATCTCCTTCCAGAAACCACCTACCGGATCAGAATTCAGGCTATAAAT
GAAATTGGAGCTGGACCATTTAGTCAGTTCATTAAAGCAAAAACTCGGCCATTACCACCCTT
GCCTCCTAGGCTAGAATGTGCTGCTGCTGGTCCTCAGAGCCTGAAGCTAAAATGGGGAGACA
GTAACTCCAAGACACATGCTGCTGAGGACATTGTGTACACACTACAGCTGGAGGACAGAAAC
AAGAGGTTTATTTCAATCTACAGAGGACCCAGCCACACCTACAAGGTCCAGAGACTGACGGA
ATTCACATGCTACTCCTTCAGAATCCAGGCAGCAAGCGAGGCTGGAGAAGGGCCCTTCTCAG
AAACCTATACCTTCAGCACAACCAAAAGTGTCCCCCCCACCATCAAAGCACCTCGAGTAACA
CAGTTAGAAGTAAATTCATGTGAAATTTTATGGGAGACGGTACCATCAATGAAAGGTGACCC
TGTTAACTACATTCTGCAGGTATTGGTTGGAAGAGAATCTGAGTACAAACAGGTGTACAAGG
GAGAAGAAGCCACATTCCAAATCTCAGGCCTCCAGACCAACACAGACTACAGGTTCCGCGTA
TGTGCGTGTCGTCGCTGTTTAGACACCTCTCAGGAGCTAAGCGGAGCCTTCAGCCCCTCTGC
GGCTTTTGTATTACAACGAAGTGAGGTCATGCTTACAGGGGACATGGGGAGCTTAGATGATC
CCAAAATGAAGAGCATGATGCCTACTGATGAACAGTTTGCAGCCATCATTGTGCTTGGCTTT
GCAACTTTGTCCATTTTATTTGCCTTTATATTACAGTACTTCTTAATGAAG**TAA**ACCCAACA
AAACTAGAGGTATGAATTAATGCTACACATTTTAATACACACATTTATTCAGATACTCCCCT
TTTTAAAGCCCTTTTGTTTTTTGATTTATATACTCTGTTTTACAGATTTAGCTAGAAAAAAA
ATGTCAGTGTTTTGGTGCACCTTTTTGAAATGCAAAACTAGGAAAAGGTTAAACTGGATTTT
TTTTTAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 94

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA191064
><subunit 1 of 1, 847 aa, 1 stop
><MW: 93607, pI: 5.33, NX(S/T): 3
MYNSVKGSCSEPVSFTTHSCAPECPFPPKLAHRSKSSLTLQWKAPIDNGSKITNYLLEWD
EGKRNSGFRQCFFGSQKHCKLTKLCPAMGYTFRLAARNDIGTSGYSQEVVCYTLGNIPQM
PSALRLVRAGITWVTLQWSKPEGCSPEEVITYTLEIQEDENDNLFHPKYTGEDLTCTVKN
LKRSTQYKFRLTASNTEGKSCPSEVLVCTTSPDRPGPPTRPLVKGPVTSHGFSVKWDPPK
DNGGSEILKYLLEITDGNSEANQWEVAYSGSATEYTFTHLKPGTLYKLRACCISTGGHSQ
CSESLPVRTLSIAPGQCRPPRVLGRPKHKEVHLEWDVPASESGCEVSEYSVEMTEPEDVA
SEVYHGPELECTVGNLLPGTVYRFRVRALNDGGYGPYSDVSEITTAAGPPGQCKAPCISC
TPDGCVLVGWESPDSSGADISEYRLEWGEDEESLELIYHGTDTRFEIRDLLPAAQYCCRL
QAFNQAGAGPYSELVLCQTPASAPDPVSTLCVLEEEPLDAYPDSPSACLVLNWEEPCNNG
SEILAYTIDLGDTSITVGNTTMHVMKDLLPETTYRIRIQAINEIGAGPFSQFIKAKTRPL
PPLPPRLECAAAGPQSLKLKWGDSNSKTHAAEDIVYTLQLEDRNKRFISIYRGPSHTYKV
QRLTEFTCYSFRIQAASEAGEGPFSETYTFSTTKSVPPTIKAPRVTQLEVNSCEILWETV
PSMKGDPVNYILQVLVGRESEYKQVYKGEEATFQISGLQTNTDYRFRVCACRRCLDTSQE
LSGAFSPSAAFVLQRSEVMLTGDMGSLDDPKMKSMMPTDEQFAAIIVLGFATLSILFAFI
LQYFLMK

**Important features of the protein:**
**Transmembrane domain:**
Amino acids 823-843

**N-glycosylation sites:**
Amino acids 48-51;539-542;559-562

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 63-66;182-185

**Tyrosine kinase phosphorylation sites:**
Amino acids 387-394;662-669

**N-myristoylation sites:**
Amino acids 49-54;257-262;343-348;437-442;757-762

**Amidation site:**
Amino acids 61-64

**ATP/GTP-binding site motif A (P-loop):**
Amino acids 193-200

**Fibronectin type III domain:**
Amino acids 22-106;118-203;215-302;314-398;
410-492;504-590;601-685;697-778

# FIGURE 95A

CAATTCGGCCTCGCTCCTTGTGATTGCGCTAAACCTTCCGTCCTCAGCTGAGAACGCTCCACCACCTCCCCGGA
TCGCTCATCTCTTGGCTGCCCTCCCACTGTTCCTGATGTTATTTTACTCCCCGTATCCCCTACTCGTTCTTCAC
AATTCTGTAGGTGAGTGGTTCCAGCTGGTGCCTGGCCTGTGTCTCTTGGATGCCCTGTGGCTTCAGTCCGTCTC
CTGTTGCCCACCACCTCGTCCCTGGGCCGCCTGATACCCCAGCCCAACAGCTAAGGTGTGGATGGACAGTAGGG
GGCTGGCTTCTCTCACTGGTCAGGGGTCTTCTCCCCTGTCTGCCTCCCGGAGCTAGGACTGCAGAGGGGCCTAT
CATGGTGCTTGCAGGCCCCCTGGCTGTCTCGCTGTTGCTGCCCAGCCTCACACTGCTGGTGTCCCACCTCTCCA
GCTCCCAGGATGTCTCCAGTGAGCCCAGCAGTGAGCAGCAGCTGTGCGCCCTTAGCAAGCACCCCACCGTGGCC
TTTGAAGACCTGCAGCCGTGGGTCTCTAACTTCACCTACCCTGGAGCCCGGGATTTCTCCCAGCTGGCTTTGGA
CCCCTCCGGGAACCAGCTCATCGTGGGAGCCAGGAACTACCTCTTCAGACTCAGCCTTGCCAATGTCTCTCTTC
TTCAGGCCACAGAGTGGGCCTCCAGTGAGGACACGCGCCGCTCCTGCCAAAGCAAAGGGAAGACTGAGGAGGAG
TGTCAGAACTACGTGCGAGTCCTGATCGTCGCCGGCCGGAAGGTGTTCATGTGTGGAACCAATGCCTTTTCCCC
CATGTGCACCAGCAGACAGGTGGGGAACCTCAGCCGGACTATTGAGAAGATCAATGGTGTGGCCCGCTGCCCCT
ATGACCCACGCCACAACTCCACAGCTGTCATCTCCTCCCAGGGGGAGCTCTATGCAGCCACGGTCATCGACTTC
TCAGGTCGGGACCCTGCCATCTACCGCAGCCTGGGCAGTGGGCCACCGCTTCGCACTGCCCAATATAACTCCAAG
TGGCTTAATGAGCCAAACTTCGTGGCAGCCTATGATATTGGGCTGTTTGCATACTTCTTCCTGCGGGAGAACGC
AGTGGAGCACGACTGTGGACGCACCGTGTACTCTCGCGTGGCCCGCGTGTGCAAGAATGACGTGGGGGGCCGAT
TCCTGCTGGAGGACACATGGACCACATTCATGAAGGCCCGGCTCAACTGCTCCCGCCCGGGCGAGGTCCCCTTC
TACTATAACGAGCTGCAGAGTGCCTTCCACTTGCCGGAGCAGGACCTCATCTATGGAGTTTTCACAACCAACGT
AAACAGCATCGCGGCTTCTGCTGTCTGCGCCTTCAACCTCAGTGCTATCTCCCAGGCTTTCAATGGCCCATTTC
GCTACCAGGAGAACCCCAGGGCTGCCTGGCTCCCCATAGCCAACCCCATCCCCAATTTCCAGTGTGGCACCCTG
CCTGAGACCGGTCCCAACGAGAACCTGACGGAGCGCAGCCTGCAGGACGCGCAGCGCCTCTTCCTGATGAGCGA
GGCCGTGCAGCCGGTGACACCCGAGCCCTGTGTCACCCAGGACAGCGTGCGCTTCTCACACCTCGTGGTGGACC
TGGTGCAGGCTAAAGACACGCTCTACCATGTACTCTACATTGGCACCGAGTCGGGCACCATCCTGAAGGCGCTG
TCCACGGCGAGCCGCAGCCTCCACGGCTGCTACCTGGAGGAGCTGCACGTGCTGCCCCCCGGGCGCCGCGAGCC
CCTGCGCAGCCTGCGCATCCTGCACAGCGCCCGCGCGCTCTTCGTGGGGCTGAGAGACGGCGTCCTGCGGGTCC
CACTGGAGAGGTGCGCCGCCTACCGCAGCCAGGGGGCATGCCTGGGGGCCCGGGACCCGTACTGTGGCTGGGAC
GGGAAGCAGCAACGTTGCAGCACACTCGAGGACAGCTCCAACATGAGCCTCTGGACCCAGAACATCACCGCCTG
TCCTGTGCGGAATGTGACACGGGATGGGGGCTTCGGCCCATGGTCACCATGGCAACCATGTGAGCACTTGGATG
GGGACAACTCAGGCTCTTGCCTGTGTCGAGCTCGATCCTGTGATTCCCCTCGACCCCGCTGTGGGGGCCTTGAC
TGCCTGGGGCCAGCCATCCACATCGCCAACTGCTCCAGGAATGGGGCGTGGACCCCGTGGTCATCGTGGGCGCT
GTGCAGCACGTCCTGTGGCATCGGCTTCCAGGTCCGCCAGCGAAGTTGCAGCAACCCTGCTCCCCGCCACGGGGGC
CGCATCTTCGTGGGCAAGAGCCGGGAGGAACGGTTCTGTAATGAGAACACGCCTTGCCCGGTGCCCATCTTCTG
GGCTTCCTGGGGCTCCTGGAGCAAGTGCAGCAGCAACTGTGGAGGGGGCATGCAGTCGCGGCGTCGGGCCTGCG
AGAACGGCAACTCCTGCCTGGGCTGCGGCGAGTTCAAGACGTGCAACCCCGAGGGCTGCCCCGAAGTGCGGCGC
AACACCCCCTGGACGCCGTGGCTGCCCGTGAACGTGACGCAGGGCGGGGCACGGCAGGAGCAGCGGTTCCGCTT
CACCTGCCGCGCGCCCCTTGCAGACCCGCACGGCCTGCAGTTCGGCAGGAGAAGGACCGAGACGAGGACCTGTC
CCGCGGACGGCTCCGGCTCCTGCGACACCGACGCCCTGGTGGAGGTCCTCCTGCGCAGCGGGAGCACCTCCCCG
CACACGGTGAGCGGGGGCTGGGCCGCCTGGGGCCCGTGGTCGTCCTGCTCCCGGGACTGCGAGCTGGGCTTCCG
CGTCCGCAAGAGAACGTGCACTAACCCGGAGCCCCGCAACGGGGGCCTGCCCTGCGTGGGCGATGCTGCCGAGT
ACCAGGACTGCAACCCCCAGGCTTGCCCAGTTCGGGGTGCTTGGTCCTGCTGGACCTCATGGTCTCCATGCTCA
GCTTCCTGTGGTGGGGGTCACTATCAACGCACCCGTTCCTGCACCAGCCCCGCACCCTCCCCAGGTGAGGACAT
CTGTCTCGGGCTGCACACGGAGGAGGCACTATGTGCCACACAGGCCTGCCCAGGCTGGTCGCCCTGGTCTGAGT
GGAGTAAGTGCACTGACGACGGAGCCCAGAGCCGAAGCCGGCACTGTGAGGAGCTCCTCCCAGGGTCCAGCGCC
TGTGCTGGAAACAGCAGCCAGAGCCGCCCCTGCCCCTACAGCGAGATTCCCGTCATCCTGCCAGCCTCCAGCAT
GGAGGAGGCCACCGACTGTGCAGGTAAAAGAAACCGGACCTACCTCATGCTGCGGTCCTCCCAGCCCTCCAGCA
CCCCACTCCAAAGTCTGGACTCTTTCCACATCCTGCTCCAGACAGCCAAGCTTTGTTGGGGTCCCCACTGCTTT
GAGATGGGTTCAATCTCATCCACTTGGTGGCCACGGGCATCTCCTGCTTCTTGGGCTCTGGGCTCCTGACCCTA
GCAGTGTACCTGTCTTGCCAGCACTGCCAGCGTCAGTCCCAGGAGTCCACACTGGTCCATCCTGCCACCCCCAACC
ATTTGCACTACAAGGGCGGAGGCACCCCGAAGAATGAAAAGTACACACCCATGGAATTCAAGACCCTGAACAAG
AATAACTTGATCCCTGATGACAGAGCCAACTTCTACCCATTGCAGCAGACCAATGTGTACACGACTACTTACTA
CCCAAGCCCCCTGAACAAACACAGCTTCCGGCCCGAGGCCTCACCTGGACAACGGTGCTTCCCCAACAGCTGAT
ACCGCCGTCCTGGGGACTTGGGCTTCTTGCCTTCATAAGGCACAGAGCAGATGGAGATGGGACAGTGGAGCCAG
TTTGGTTTTCTCCCTCTGCACTAGGCCAAGAACTTGCTGCCTTGCCTGTGGGGGGTCCCATCCGGCTTCAGAGA
GCTCTGGCTGGCATTGACCATGGGGGAAAGGGCTGGTTTCAGGCTGACATATGGCCGCAGGTCCAGTTCAGCCC
AGGTCTCTCATGGTTATCTTCCAACCCACTGTCACGCTGACACTATGCTGCCATGCCTGGGCTGTGGACCTACT
GGGCATTTGAGGAATTGGAGAATGGAGATGGCAAGAGGGCAGGCTTTTAAGTTTGGGTTGGAGACAACTTCCTG
TGGCCCCCACAAGCTGAGTCTGGCCTTCTCCAGCTGGCCCCAAAAAAGGCCTTTGCTACATCCTGATTATCTCT
GAAAGTAATCAATCAAGTGGCTCCAGTAGCTCTGGATTTTCTGCCAGGGCTGGGCCATTGTGGTGCTGCCCCAG
TATGACATGGGACCAAGGCCAGCGCAGGTTATCCACCTCTGCCTGGAAGTCTATACTCTACCCAGGGCATCCCT
CTGGTCAGAGGCAGTGAGTACTGGGAACTGGAGGCTGACCTGTGCTTAGAAGTCCTTTAATCTGGGCTGGTACA
GGCCTCAGCCTTGCCCTCAATGCACGAAAGGTGGCCCAGGAGAGAGGATCAATGCCATAGGAGGCAGAAGTCTG
GCCTCTGTGCCTCTATGGAGACTATCTTCCAGTTGCTGCTCAACAGAGTTGTTGGCTGAGACCTGCTTGGGAGT

# FIGURE 95B

CTCTGCTGGCCCTTCATCTGTTCAGGAACACACACACACACACACTCACACACGCACACACAATCACAATTTGC
TACAGCAACAAAAAAAGACATTGGGCTGTGGCATTATTAATTAAAGATGATATCCAGTC

# FIGURE 96

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA194909
><subunit 1 of 1, 1092 aa, 1 stop
><MW: 119324, pI: 8.13, NX(S/T): 14
MPCGFSPSPVAHHLVPGPPDTPAQQLRCGWTVGGWLLSLVRGLLPCLPPGARTAEGPIMV
LAGPLAVSLLLPSLTLLVSHLSSSQDVSSEPSSEQQLCALSKHPTVAFEDLQPWVSNFTY
PGARDFSQLALDPSGNQLIVGARNYLFRLSLANVSLLQATEWASSEDTRRSCQSKGKTEE
ECQNYVRVLIVAGRKVFMCGTNAFSPMCTSRQVGNLSRTIEKINGVARCPYDPRHNSTAV
ISSQGELYAATVIDFSGRDPAIYRSLGSGPPLRTAQYNSKWLNEPNFVAAYDIGLFAYFF
LRENAVEHDCGRTVYSRVARVCKNDVGGRFLLEDTWTTFMKARLNCSRPGEVPFYYNELQ
SAFHLPEQDLIYGVFTTNVNSIAASAVCAFNLSAISQAFNGPFRYQENPRAAWLPIANPI
PNFQCGTLPETGPNENLTERSLQDAQRLFLMSEAVQPVTPEPCVTQDSVRFSHLVVDLVQ
AKDTLYHVLYIGTESGTILKALSTASRSLHGCYLEELHVLPPGRREPLRSLRILHSARAL
FVGLRDGVLRVPLERCAAYRSQGACLGARDPYCGWDGKQQRCSTLEDSSNMSLWTQNITA
CPVRNVTRDGGFGPWSPWQPCEHLDGDNSGSCLCRARSCDSPRPRCGGLDCLGPAIHIAN
CSRNGAWTPWSSWALCSTSCGIGFQVRQRSCSNPAPRHGGRIFVGKSREERFCNENTPCP
VPIFWASWGSWSKCSSNCGGGMQSRRRACENGNSCLGCGEFKTCNPEGCPEVRRNTPWTP
WLPVNVTQGGARQEQRFRFTCRAPLADPHGLQFGRRRTETRTCPADGSGSCDTDALVEVL
LRSGSTSPHTVSGGWAAWGPWSSCSRDCELGFRVRKRTCTNPEPRNGGLPCVGDAAEYQD
CNPQACPVRGAWSCWTSWSPCSASCGGGHYQRTRSCTSPAPSPGEDICLGLHTEEALCAT
QACPGWSPWSEWSKCTDDGAQSRSRHCEELLPGSSACAGNSSQSRPCPYSEIPVILPASS
MEEATDCAGKRNRTYLMLRSSQPSSTPLQSLDSFHILLQTAKLCWGPHCFEMGSISSTWW
PRASPASWALGS

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-42

**Transmembrane domain:**
Amino acids 56-79;373-395

**N-glycosylation sites:**
Amino acids 117-120;153-156;215-218;236-239;345-348;391-394;
436-439;590-593;597-600;605-608;660-663;785-788;
1000-1003;1032-1035

**cAMP- and cGMP-dependent protein kinase phosphorylation sites:**
Amino acids 773-776;815-818;875-878

**Tyrosine kinase phosphorylation site:**
Amino acids 177-185;348-355

**N-myristoylation sites:**
Amino acids 42-47;50-55;373-378;492-497;543-548;563-568;
630-635;647-652;740-745;810-815;827-832;829-834;
853-858;887-892;910-915;993-998;1073-1078

**Amidation sites:**
Amino acids 192-195;522-525;813-816;1028-1031

**ATP/GTP-binding site motif A (P-loop):**
Amino acids 700-707

**Cytochrome c oxidase subunit II, copper A binding region signature:**
Amino acids 921-929

**Growth factor and cytokines receptors family signature 2:**
Amino acids 967-973

**Sema domain:**
Amino acids 126-537

**Plexin repeat:**
Amino acids 555-602

**Thrombospondin type 1 domain:**
Amino acids 613-661;668-719;726-769;856-906;913-963;967-1007

# FIGURE 97

CAAGCCCTCCCAGCATCCCCTCTCCTGTGTTCCTCCCCAGTTCTCTACTCAGAGTTGACTGACCAGAGATTTAT
CAGCTTGGAGGGCTGGAGGTGTGGATCCATGGGGTAGCCTCAACGCATCTGCCCCTCCACCCCAGCCAGCTCAT
GGGCCACGTGGCCTGGCCCAGCCTCAGCACCCAGGGCCAGTGAACAGAGCCCTGGCTGGAGTCCAAACATGTGG
GGCCTGGTGAGGCTCCTGCTGGCCTGGCTGGGTGGCTGGGGCTGCATGGGGCGTCTGGCAGCCCCAGCCCGGGC
CTGGGCAGGGTCCCGGGAACACCCAGGGCCTGCTCTGCTGCGGACTCGAAGGAGCTGGGTCTGGAACCAGTTCT
TTGTCATTGAGGAATATGCTGGTCCAGAGCCTGTTCTCATTGGCAAGCTGCACTCGGATGTTGACCGGGGAGAG
GGCCGCACCAAGTACCTGTTGACCGGGGAGGGGGCAGGCACCGTATTTGTGATTGATGAGGCCACAGGCAATAT
TCATGTTACCAAGAGCCTTGACCGGGAGGAAAAGGCGCAATATGTGCTACTGGCCCAAGCCGTGGACCGAGCCT
CCAACCGGCCCCTGGAGCCCCCATCAGAGTTCATCATCAAAGTGCAAGACATCAACGACAATCCACCCATTTTT
CCCCTTGGGCCCTACCATGCCACCGTGCCCGAGATGTCCAATGTCGGGACATCAGTGATCCAGGTGACTGCTCA
CGATGCTGATGACCCCAGCTATGGGAACAGTGCCAAGCTGGTGTACACTGTTCTGGATGGACTGCCTTTCTTCT
CTGTGGACCCCCAGACTGGAGTGGTGCGTACAGCCATCCCCAACATGGACCGGGAGACACAGGAGGAGTTCTTG
GTGGTGATCCAGGCCAAGGACATGGGCGGCCACATGGGGGGGCTGTCAGGCAGCACTACGGTGACTGTCACGCT
CAGCGATGTCAACGACAACCCCCCCAAGTTCCCACAGAGCCTATACCAGTTCTCCGTGGTGGAGACAGCTGGAC
CTGGCACACTGGTGGGCCGGCTCCGGGCCCAGGACCCAGACCTGGGGGACAACGCCCTGATGGCATACAGCATC
CTGGATGGGGAGGGGTCTGAGGCCTTCAGCATCAGCACAGACTTGCAGGGTCGAGACGGGCTCCTCACTGTCCG
CAAGCCCCTAGACTTTGAGAGCCAGCGCTCCTACTCCTTCCGTGTCGAGGCCACCAACACGCTCATTGACCCAGCC
TATCTGCGGCGAGGGCCCTTCAAGGATGTGGCCTCTGTGCGTGTGGCAGTGCAAGATGCCCCAGAGCCACCTGC
CTTCACCCAGGCTGCCTACCACCTGACAGTGCCTGAGAACAAGGCCCCGGGGACCCTGGTAGGCCAGATCTCCG
CGGCTGACCTGGACTCCCCTGCCAGCCCAATCAGATACTCCATCCTCCCCCACTCAGATCCGGAGCGTTGCTTC
TCTATCCAGCCCGAGGAAGGCACCATCCATACAGCAGCACCCCTGGATCGCGAGGCTCGCGCCTGGCACAACCT
CACTGTGCTGGCTACAGAGCTCGACAGTTCTGCACAGGCCTCGCGCGTGCAAGTGGCCATCCAGACCCTGGATG
AGAATGACAATGCTCCCCAGCTGGCTGAGCCCTACGATACTTTTGTGTGTGACTCTGCAGCTCCTGGCCAGCTG
ATTCAGGTCATCCGGGCCCTGGACAGAGATGAAGTTGGCAACAGTAGCCATGTCTCCTTTCAAGGTCCTCTGGG
CCCTGATGCCAACTTTACTGTCCAGGACAACCGAGATGGCTCCGCCAGCCTGCTGCTGCCCTCCCGCCCTGCTC
CACCCCGCCATGCCCCCTACTTGGTTCCCATAGAACTGTGGGACTGGGGGCAGCCGGCGCTGAGCAGCACTGCC
ACAGTGACTGTTAGTGTGTGCCGCTGCCAGCCTGACGGCTCTGTGGCATCCTGCTGGCCTGAGGCTCACCTCTC
AGCTGCTGGGCTCAGCACCGGCGCCCTGCTTGCCATCATCACCTGTGTGGGTGCCCTGCTTGCCCTGGTGGTGC
TCTTCGTGGCCCTGCGGCGGCAGAAGCAAGAAGCACTGATGGTACTGGAGGAGGAGGACGTCCGAGAGAACATC
ATCACCTACGACGACGAGGGCGGCGGCGAGGAGGACACCGAGGCCTTCGACATCACGGCCTTGCAGAACCCGGA
CGGGGCGGCCCCCCCGGCGCCCGGCCCTCCCGCGCGCCGAGACGTGTTGCCCCGGGCCCGGGTGTCGCGCCAGC
CCAGACCCCCCGGCCCCGCCGACGTGGCGCAGCTCCTGGCGCTGCGGCTCCGCGAGGCGGACGAGGACCCCGGC
GTACCCCCGTACGACTCGGTGCAGGTGTACGGCTACGAGGGCCGCGGCTCCTCTTGCGGCTCCCTCAGCTCCCT
GGGCTCCGGCAGCGAAGCCGGCGGCGCCCCCGGCCCCGCGGAGCCGCTGGACGACTGGGGTCCGCTCTTCCGCACC
CTGGCCGAGCTGTATGGGGCCAAGGAGCCCCCGGCCCCCTGAGCGCCCGGGCTGGCCCGGCCCACCGCGGGGGG
GGGGCAGCGGGCACAGGCCCTCTGAGTGAGCCCCACGGGGTCCAGGCGGGCGGCAGCAGCCCAGGGGCCCCAGG
CCTCCTCCCTGTCCTTGTGTCCCTCCTTGCTTCCCCGGGGCACCCTCGCTCTCACCTCCCTCCTCCTGAGTCGG
TGTGTGTGTCTCTCTCCAGGAATCTTTGTCTCTATCTGTGACACGCTCCTCTGTCCGGGCCTGGGTTTCCTGCC
CTGGCCCTGGCCCTGCGATCTCTCACTGTGATTCCTCTCCTTCCTCCGTGGCGTTTTGTCTCTGCAGTTCTGAA
GCTCACACATAGTCTCCCTGCGTCTTCCTTGCCCATACACATGCTCTGTGTCTGTCTCCTGCCCACATCTCCCT
TCCTTCTCTCTGGGTCCCTGTGACTGGCTTTTTGTTTTTTTCTGTTGTCCATCCCAAAATCAAGAGAAACTTCC
AGCCACTGCTGCCCACCCTCCTGCAGGGGATGTTGTGCCCCAGACCTGCCTGCATGGTTCCATCCATTACTCAT
GGCCTCAGCCTCATCCTGGCTCCACTGGCCTCCAGCTGAGAGAGGGAACCAGCCTGCCTCCCAGGGCAAGAGCT
CCAGCCTCCCGTGTGGCCGCCTCCCTGGAGCTCTGCCCAGCTGCCAGCTTCCCCTGGGCATCCCAGCCCTGGGC
ATTGTCTTGTGTGCTTCCTGAGGGAGTAGGGAAAGGAAAGGGGGAGGCGGCTGGGGAAGGGGAAAGAGGGAGGA
AGGGGAGGGGCCTCCATCTCTAATTTCATAATAAACAAACACTTTATTTTGTAAAAC

# FIGURE 98

MWGLVRLLLAWLGGWGCMGRLAAPARAWAGSREHPGPALLRTRRSWVWNQFFVIEEYAGP
EPVLIGKLHSDVDRGEGRTKYLLTGEGAGTVFVIDEATGNIHVTKSLDREEKAQYVLLAQ
AVDRASNRPLEPPSEFIIKVQDINDNPPIFPLGPYHATVPEMSNVGTSVIQVTAHDADDP
SYGNSAKLVYTVLDGLPFFSVDPQTGVVRTAIPNMDRETQEEFLVVIQAKDMGGHMGGLS
GSTTVTVTLSDVNDNPPKFPQSLYQFSVVETAGPGTLVGRLRAQDPDLGDNALMAYSILD
GEGSEAFSISTDLQGRDGLLTVRKPLDFESQRSYSFRVEATNTLIDPAYLRRGPFKDVAS
VRVAVQDAPEPPAFTQAAYHLTVPENKAPGTLVGQISAADLDSPASPIRYSILPHSDPER
CFSIQPEEGTIHTAAPLDREARAWHNLTVLATELDSSAQASRVQVAIQTLDENDNAPQLA
EPYDTFVCDSAAPGQLIQVIRALDRDEVGNSSHVSFQGPLGPDANFTVQDNRDGSASLLL
PSRPAPPRHAPYLVPIELWDWGQPALSSTATVTVSVCRCQPDGSVASCWPEAHLSAAGLS
TGALLAIITCVGALLALVVLFVALRRQKQEALMVLEEEDVRENIITYDDEGGGEEDTEAF
DITALQNPDGAAPPAPGPPARRDVLPRARVSRQPRPPGPADVAQLLALRLREADEDPGVP
PYDSVQVYGYEGRGSSCGSLSSLGSGSEAGGAPGPAEPLDDWGPLFRTLAELYGAKEPPA
P

**Signal peptide:**
Amino acids 1-16

**Transmembrane domain:**
Amino acids 597-624

**N-glycosylation sites:**
Amino acids 446-449;510-513;525-528

**N-myristoylation sites:**
Amino acids 13-18;206-211;233-238;237-242;238-243;275-280;390-395;
394-399;429-434;583-588;598-603;602-607;612-617;
734-739;738-743;746-751

**ATP synthase c subunit signature:**
Amino acids 691-712

**Cadherins extracellular repeated domain signature:**
Amino acids 138-148;247-257

**Cadherin domain:**
Amino acids 50-141;155-250;264-366;379-470;483-577

**Cadherin cytoplasmic region:**
Amino acids 625-776

# FIGURE 99

GCCAACACTGGCCAAACATATGGGGCTGGAATCTCAACATCGGTCACTGGGACCTCAATATT
TGGAGCCGGAACCCCACAATTTGGAACACAGACCCCAATATTTGGAGCAGAACCCCAAGATT
TGACATCTAAAACCTCAAGCCTGGAGCTGAACTCTGAATTCTGGGCCTGGGACCTTGAAATC
TGGGACTGGATTTCCAGTACTGTACCCTGGAACCCACTCTTGGGGACCTGAACCCTGGGATT
CAGGCCTCAAATTCCAAGATCTGGACTGTGGGATTCCAAGGGGCCTGAACCCGAGTTTGGGC
CTGAAGTCCTTGCTGCAGACCTGAGTGCTTAAATCTGGGGCTTGAGACCTCCCAATCTTGAC
TCAGCACCCCAATATCTGAATGCAGAACCCCGGGATCGGATCTCAGACTCTAAACCCCACCG
TTTGGCTGCTTAGCATCCCAAGACTGGACCTGGGAGACCCTGACCCTGAACAACCCAAACTG
GACCCGTAAAACTGGACCCTAGAGGCCCAATATTTAGGGGTCTGGAACCCCGAGTATTAAGG
TCTGGAGACTCCGTTGCCACAGATTTGAGCCGAGTCAGGACACAGTCCCTCTACAGAAGCCT
TGGGGACAGGAAAAGCATGACCAGATGCTCCCTCCAGAGCCCTGACCTCTGACTCCCCTGGA
GCTAGGACTCTGCTCCCTGGGGCTGCTTCTAGCTCAGGACACCCCTGCCCGCG**ATG**GCCATC
CTCCCGTTGCTCCTGTGCCTGCTGCCGCTGGCCCCTGCCTCATCCCCACCCCAGTCAGCCAC
ACCCAGCCCATGTCCCCGCCGCTGCCGCTGCCAGACACAGTCGCTGCCCCTAAGCGTGCTGT
GCCCAGGGGCAGGCCTCCTGTTCGTGCCACCCTCGCTGGACCGCCGGGCAGCCGAGCTGCGG
CTGGCAGACAACTTCATCGCCTCCGTGCGCCGCCGCGACCTGGCCAACATGACAGGCCTGCT
GCATCTGAGCCTGTCGCGGAACACCATCCGCCACGTGGCTGCCGGCGCCTTCGCCGACCTGC
GGGCCCTGCGTGCCCTGCACCTGGATGGCAACCGGCTGACCTCACTGGGCGAGGGCCAGCTG
CGCGGCCTGGTCAACTTGCGCCACCTCATCCTCAGCAACAACCAGCTGGCAGCGCTGGCGGC
CGGCGCCCTGGATGATTGTGCCGAGACACTGGAGGACCTCGACCTCTCCTACAACAACCTCG
AGCAGCTGCCCTGGGAGGCCCTGGGCCGCCTGGGCAACGTCAACACGTTGGGCCTCGACCAC
AACCTGCTGGCTTCTGTGCCCGGCGCTTTTTCCCGCCTGCACAAGCTGGCCCGGCTGGACAT
GACCTCCAACCGCCTGACCACAATCCCACCCGACCCACTCTTCTCCCGCCTGCCCCTGCTCG
CCAGGCCCCGGGGCTCGCCCGCCTCTGCCCTGGTGCTGGCCTTTGGCGGGAACCCCCTGCAC
TGCAACTGCGAGCTGGTGTGGCTGCGTCGCCTGGCGCGGGAGGACGACCTCGAGGCCTGCGC
GTCCCCACCTGCTCTGGGCGGCCGCTACTTCTGGGCGGTGGGCGAGGAGGAGTTTGTCTGCG
AGCCGCCCGTGGTGACTCACCGCTCACCACCTCTGGCTGTGCCCGCAGGTCGGCCGGCTGCC
CTGCGCTGCCGGGCAGTGGGGGACCCAGAGCCCCGTGTGCGTTGGGTGTCACCCCAGGGCCG
GCTGCTAGGCAACTCAAGCCGTGCCCGCGCCTTCCCCAATGGGACGCTGGAGCTGCTGGTCA
CCGAGCCGGGTGATGGTGGCATCTTCACCTGCATTGCGGCCAATGCAGCTGGCGAGGCCACA
GCTGCTGTGGAGCTGACTGTGGGTCCCCCACCACCTCCTCAGCTAGCCAACAGCACCAGCTG
TGACCCCCCGCGGGACGGGGATCCTGATGCTCTCACCCCACCCTCCGCTGCCTCTGCTTCTG
CCAAGGTGGCCGACACTGGGCCCCCTACCGACCGTGGCGTCCAGGTGACTGAGCACGGGGCC
ACAGCTGCTCTTGTCCAGTGGCCGGATCAGCGGCCTATCCCGGGCATCCGCATGTACCAGAT
CCAGTACAACAGCTCGGCTGATGACATCCTCGTCTACAGGATGATCCCGGCGGAGAGCCGCT
CGTTCCTGCTGACGGACCTGGCGTCAGGCCGGACCTACGATCTGTGCGTGCTCGCCGTGTAT
GAGGACAGCGCCACGGGGCTCACGGCCACGCGGCCTGTGGGCTGCGCCCGCTTCTCCACCGAA
CCTGCGCTGCGGCCATGCGGGGCGCCGCACGCTCCCTTCCTGGGCGGCACGATGATCATCGC
GCTGGGCGGCGTCATCGTAGCCTCGGTACTGGTCTTCATCTTCGTGCTGCTAATGCGCTACA
AGGTGCACGGCGGCCAGCCCCCCGGCAAGGCCAAGATTCCCGCGCCTGTTAGCAGCGTTTGC
TCCCAGACCAACGGCGCCCTGGGCCCCACGCCCACGCCCGCCCCGCCCGCCCCGGAGCCCGC
GGCGCTCAGGGCCCACACCGTGGTCCAGCTGGACTGCGAGCCCTGGGGGCCCGGCCACGAAC
CTGTGGGACCC**TAG**CCAGGCGCCCCCCCCTCTAAGGGTCCTCTGGCCCCACGGACAGCAGGA
CCCGGACACCCTGTGGGACCTGGCCTCAAACTCACCAAATCGCTCATGGTTTTTAAAACTCT
GATGGGGAGGGTGTCGGGGACACCGGGGCAAAACAAGAAAGTCCTATTTTTCCAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 100

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA213858
><subunit 1 of 1, 627 aa, 1 stop
><MW: 66189, pI: 7.31, NX(S/T): 5
MAILPLLLCLLPLAPASSPPQSATPSPCPRRCRCQTQSLPLSVLCPGAGLLFVPPSLDRR
AAELRLADNFIASVRRRDLANMTGLLHLSLSRNTIRHVAAGAFADLRALRALHLDGNRLT
SLGEGQLRGLVNLRHLILSNNQLAALAAGALDDCAETLEDLDLSYNNLEQLPWEALGRLG
NVNTLGLDHNLLASVPGAFSRLHKLARLDMTSNRLTTIPPDPLFSRLPLLARPRGSPASA
LVLAFGGNPLHCNCELVWLRRLAREDDLEACASPPALGGRYFWAVGEEEFVCEPPVVTHR
SPPLAVPAGRPAALRCRAVGDPEPRVRWVSPQGRLLGNSSRARAFPNGTLELLVTEPGDG
GIFTCIAANAAGEATAAVELTVGPPPPPQLANSTSCDPPRDGDPDALTPPSAASASAKVA
DTGPPTDRGVQVTEHGATAALVQWPDQRPIPGIRMYQIQYNSSADDILVYRMIPAESRSF
LLTDLASGRTYDLCVLAVYEDSATGLTATRPVGCARFSTEPALRPCGAPHAPFLGGTMII
ALGGVIVASVLVFIFVLLMRYKVHGGQPPGKAKIPAPVSSVCSQTNGALGPTPTPAPPAP
EPAALRAHTVVQLDCEPWGPGHEPVGP

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-16

**Transmembrane domain:**
Amino acids 35-55; 536-556

**N-glycosylation sites:**
Amino acids 81-84;338-341;347-350;392-395;461-464

**N-myristoylation sites:**
Amino acids 116-121;125-130;180-185;186-191;235-240;
360-365;361-366;429-434;436-441;505-510;
544-549;566-571

**Leucine Rich Repeat:**
Amino acids 60-83;84-107;108-131;132-155;157-180;
181-203;204-227

**Leucine rich repeat C-terminal domain:**
Amino acids 248-293

**Immunoglobulin domain:**
Amino acids 309-367

**Fibronectin type III domain:**
Amino acids 424-504

# FIGURE 101

CGACTCCATAACCGTGGCCTTGGCCCCAGTCCCCCTGACTTCCGGACTTCAGACCAGATACTGCCCATATCCCC
TTATGAAGTCTTGGCCAGGCAACCCCTAGGGTGTACGTTTTCTAAAGATTAAAGAGGCGGTGCTAAGCTGCAGA
CGGACTTGCGACTCAGCCACTGGTGTAAGTCAGGCGGGAGGTGGCGCCCAATAAGCTCAAGAGAGGAGGCGGGT
TCTGGAAAAAGGCCAATAGCCTGTGAAGGCGAGTCTAGCAGCAACCAATAGCTATGAGCGAGAGGCGGGACTCT
GAGGGAAGTCAATCGCTGCCGCAGGTACCGCCAATGGCTTTTGGCGGGGGCGTTCCCCAACCCTGCCCTCTCTC
ATGACCCCGCTCCGGGATTATGGCCGGGACTGGGCTGCTGGCGCTGCGGACGCTGCCAGGGCCCAGCTGGGTGC
GAGGCTCGGGCCCTTCCGTGCTGAGCCGCCTGCAGGACGCGGCCGTGGTGCGGCCTGGCTTCCTGAGCACGGCA
GAGGAGGAGACGCTGAGCCGAGAACTGGAGCCCGAGCTGCGCCGCCGCCGCTACGAATACGATCACTGGGACGC
GGCCATCCACGGCTTCCGAGAGACAGAGAAGTCGCGCTGGTCAGAAGCCAGCCGGGCCATCCTGCAGCGCGTGC
AGGCGGCCGCCTTTGGCCCCGGCCAGACCCTGCTCTCCTCCGTGCACGTGCTGGACCTGGAAGCCCGCGGCTAC
ATCAAGCCCCACGTGGACAGCATCAAGTTCTGCGGGGCCACCATCGCCGGCCTGTCTCTCCTGTCTCCCAGCGT
TATGCGGCTGGTGCACACCCAGGAGCCGGGGGAGTGGCTGGAACTCTTGCTGGAGCCGGGCTCCCTCTACATCC
TTAGGGGCTCAGCCCGTTATGACTTCTCCCATGAGATCCTTCGGGATGAAGAGTCCTTCTTTGGGGAACGCCGG
ATTCCCCGGGGCCGGCGCATCTCCGTGATCTGCCGCTCCCTCCCTGAGGGCATGGGGCCAGGGGAGTCTGGACA
GCCGCCCCCAGCCTGCTGACCCCCAGCTTTCTACAGACACCAGATTTGTGAATAAAGTTGGGGAATGGACAGCCT

# FIGURE 102

MAGTGLLALRTLPGPSWVRGSGPSVLSRLQDAAVVRPGFLSTAEEETLSRELEPELRRRRYEYDHWDAAIHGFR
ETEKSRWSEASRAILQRVQAAAFGPGQTLLSSVHVLDLEARGYIKPHVDSIKFCGATIAGLSLLSPSVMRLVHT
QEPGEWLELLLEPGSLYILRGSARYDFSHEILRDEESFFGERRIPRGRRISVICRSLPEGMGPGESGQPPPAC

Important features of the protein:

Signal peptide:
1-18

Transmembrane domain:
None

cAMP- and cGMP-dependent protein kinase phosphorylation site.
196-199

N-myristoylation site.
20-25
129-134
208-213

Amidation site.
194-197

# FIGURE 103

CTCCCCGGCGCCGCAGGCAGCGTCCTCCTCCGAAGCAGCTGCACCTGCAACTGGGCAGCCTGGACCCTCGTGCC
CTGTTCCCGGGACCTCGCGCAGGGGGCGCCCCGGGACACCCCCTGCGGGCCGGGTGGAGGAGGAAGAGGAGGAG
GAGGAAGAAGACGTGGACAAGGACCCCCATCCTACCCAGAACACCTGCCTGCGCTGCCGCCACTTCTCTTTAAG
GGAGAGGAAAAGAGAGCCTAGGAGAACCATGGGGGGCTGCGAAGTCCGGGAATTTCTTTTGCAATTTGGTTTCT
TCTTGCCTCTGCTGACAGCGTGGCCAGGCGACTGCAGTCACGTCTCCAACAACCAAGTTGTGTTGCTTGATACA
ACAACTGTACTGGGAGAGCTAGGATGGAAAACATATCCATTAAATGGGTGGGATGCCATCACTGAAATGGATGA
ACATAATAGGCCCATTCACACATACCAGGTATGTAATGTAATGGAACCAAACCAAAACAACTGGCTTCGTACAA
ACTGGATCTCCCGTGATGCAGCTCAGAAAATTTATGTGGAAATGAAATTCACACTAAGGGATTGTAACAGCATC
CCATGGGTCTTGGGGACTTGCAAAGAAACATTTAATCTGTTTTATATGGAATCAGATGAGTCCCACGGAATTAA
ATTCAAGCCAAACCAGTATACAAAGATCGACACAATTGCTGCTGATGAGAGTTTTACCCAGATGGATTTGGGTG
ATCGCATCCTCAAACTCAACACTGAAATTCGTGAGGTGGGGCCTATAGAAAGGAAAGGATTTTATCTGGCTTTT
CAAGACATTGGGGCGTGCATTGCCCTGGTTTCAGTCCGTGTTTTCTACAAGAAATGCCCCTTCACTGTTCGTAA
CTTGGCCATGTTTCCTGATACCATTCCAAGGGTTGATTCCTCCTCTTTGGTTGAAGTACGGGGTTCTTGTGTGA
AGAGTGCTGAAGAGCGTGACACTCCTAAACTGTATTGTGGAGCTGATGGAGATTGGCTGGTTCCTCTTGGAAGG
TGCATCTGCAGTACAGGATATGAAGAAATTGAGGGTTCTTGCCATGCTTGCAGACCAGGATTCTATAAAGCTTT
TGCTGGGAACACAAAATGTTCTAAATGTCCTCCACACAGTTTAACATACATGGAAGCAACTTCTGTCTGTCAGT
GTGAAAAGGGTTATTTCCGAGCTGAAAAAGACCCACCTTCTATGGCATGTACCAGGCCACCTTCAGCTCCTAGG
AATGTGGTTTTTAACATCAATGAAACAGCCCTTATTTTGGAATGGAGCCCACCAAGTGACACAGGAGGGAGAAA
AGATCTCACATACAGTGTAATCTGTAAGAAATGTGGCTTAGACACCAGCCAGTGTGAGGACTGTGGTGGAGGAC
TCCGCTTCATCCCAAGACATACAGGCCTGATCAACAATTCCGTGATAGTACTTGACTTTGTGTCTCACGTGAAT
TACACCTTTGAAATAGAAGCAATGAATGGAGTTTCTGAGTTGAGTTTTTCTCCCAAGCCATTCACAGCTATTAC
AGTGACCACGGATCAAGATGCACCTTCCCTGATAGGTGTGGTAAGGAAGGACTGGGCATCCCAAAATAGCATTGCC
CTATCATGGCAAGCACCTGCTTTTTCCAATGGAGCCATTCTGGACTACGAGATCAAGTACTATGAGAAAGAACA
TGAGCAGCTGACCTACTCTTCCACAAGGTCCAAAGCCCCCAGTGTCATCATCACAGGTCTTAAGCCAGCCACCA
AATATGTATTTCACATCCGAGTGAGAACTGCGACAGGATACAGTGGCTACAGTCAGAAATTTGAATTTGAAACA
GGAGATGAAACTTCTGACATGGCAGCAGAACAAGGACAGATTCTCGTGATAGCCACCGCCGCTGTTGGCGGATT
CACTCTCCTCGTCATCCTCACTTTATTCTTCTTGATCACTGGGAGATGTCAGTGGTACATAAAAGCCAAGATGA
AGTCAGAAGAGAAGAGAAGAAACCACTTACAGAATGGGCATTTGCGCTTCCCGGGAATTAAAACTTACATTGAT
CCAGATACATATGAAGACCCATCCCTAGCAGTCCATGAATTTGCAAAGGAGATTGATCCCTCAAGAATTCGTAT
TGAGAGAGTCATTGGGGCAGGTGAATTTGGAGAAGTCTGTAGTGGGCGTTTGAAGACACCAGGGAAAAGAGAGA
TCCCAGTTGCCATTAAAACTTTGAAAGGTGGCCACATGGATCGGCAAAGAAGAGATTTTCTAAGAGAAGCTAGT
ATCATGGGCCAGTTTGACCATCCAAACATCATTCGCCTAGAAGGGGTTGTCACCAAAAGATCCTTCCCGGCCAT
TGGGGTGGAGGCGTTTTGCCCCAGCTTCCTGAGGGCAGGGTTTTTAAATAGCATCCAGGCCCCGCATCCAGTGC
CAGGGGGAGGATCTTTGCCCCCCAGGATTCCTGCTGGCAGACCAGTAATGATTGTGGTGGAATATATGGAGAAT
GGATCCCTAGACTCCTTTTTGCGGAAGCATGATGGCCACTTCACAGTCATCCAGTTGGTCGGAATGCTCCGAGG
CATTGCATCAGGCATGAAGTATCTTTCTGATATGGGTTATGTTCATCGAGACCTAGCGGCTCGGAATATACTGG
TCAATAGCAACTTAGTATGCAAAGTTTCTGATTTTGGTCTCTCCAGAGTGCTGGAAGATGATCCAGAAGCTGCT
TATACAACAACTGGTGGAAAAATCCCCATAAGGTGGACAGCCCCAGAAGCCATCGCCTACAGAAAATTCTCCTC
AGCAAGCGATGCATGGAGCTATGGCATTGTCATGTGGGAGGTCATGTCCTATGGAGAGAGACCTTATTGGGAAATG
TCTAACCAAGATGTCATTCTGTCCATTGAAGAAGGGTACAGACTTCCAGCTCCCATGGGCTGTCCAGCATCTCT
ACACCAGCTGATGCTCCACTGCTGGCAGAAGGAGAGAAATCACAGACCAAAATTTACTGACATTGTCAGCTTCC
TTGACAAACTGATCCGAAATCCCAGTGCCCTTCACACCCTGGTGGAGGACATCCTTGTAATGCCAGAGTCCCCT
GGTGAAGTTCCGGAATATCCTTTGTTTGTCACAGTTGGTGACTGGCTAGATTCTATAAAGATGGGGCAATACAA
GAATAACTTCGTGGCAGCAGGGTTTACAACATTTGACCTGATTTCAAGAATGAGCATTGATGACATTAGAAGAA
TTGGAGTCATACTTATTGGACACCAGAGACGAATAGTCAGCAGCATACAGACTTTACGTTTACACATGATGCAC
ATACAGGAGAAGGGATTTCATGTATGAAAGTACCACAAGCACCTGTGTTTTGTGCCTCAGCATTTCTAAAATGA
ACGATATCCTCTCTACTACTCTCTCTTCTGATTCTCCAAACATCACTTCACAAACTGCAGTCTTCTGTTCAGAC
TATAGGCACACACCTTATGTTTATGCTTCCAACCAGGATTTTAAAATCATGCTACATAAATCCGTTCTGAATAA
CCTGCAACTAAAAAAAAAAAAAAAAAA

# FIGURE 104

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA222653
><subunit 1 of 1, 1036 aa, 1 stop
><MW: 116379, pI: 6.94, NX(S/T): 5
MGGCEVREFLLQFGFFLPLLTAWPGDCSHVSNNQVVLLDTTTVLGELGWKTYPLNGWDAI
TEMDEHNRPIHTYQVCNVMEPNQNNWLRTNWISRDAAQKIYVEMKFTLRDCNSIPWVLGT
CKETFNLFYMESDESHGIKFKPNQYTKIDTIAADESFTQMDLGDRILKLNTEIREVGPIE
RKGFYLAFQDIGACIALVSVRVFYKKCPFTVRNLAMFPDTIPRVDSSSLVEVRGSCVKSA
EERDTPKLYCGADGDWLVPLGRCICSTGYEEIEGSCHACRPGFYKAFAGNTKCSKCPPHS
LTYMEATSVCQCEKGYFRAEKDPPSMACTRPPSAPRNVVFNINETALILEWSPPSDTGGR
KDLTYSVICKKCGLDTSQCEDCGGGLRFIPRHTGLINNSVIVLDFVSHVNYTFEIEAMNG
VSELSFSPKPFTAITVTTDQDAPSLIGVVRKDWASQNSIALSWQAPAFSNGAILDYEIKY
YEKEHEQLTYSSTRSKAPSVIITGLKPATKYVFHIRVRTATGYSGYSQKFEFETGDETSD
MAAEQGQILVIATAAVGGFTLLVILTLFFLITGRCQWYIKAKMKSEEKRRNHLQNGHLRF
PGIKTYIDPDTYEDPSLAVHEFAKEIDPSRIRIERVIGAGEFGEVCSGRLKTPGKREIPV
AIKTLKGGHMDRQRRDFLREASIMGQFDHPNIIRLEGVVTKRSFPAIGVEAFCPSFLRAG
FLNSIQAPHPVPGGGSLPPRIPAGRPVMIVVEYMENGSLDSFLRKHDGHFTVIQLVGMLR
GIASGMKYLSDMGYVHRDLAARNILVNSNLVCKVSDFGLSRVLEDDPEAAYTTTGGKIPI
RWTAPEAIAYRKFSSASDAWSYGIVMWEVMSYGERPYWEMSNQDVILSIEEGYRLPAPMG
CPASLHQLMLHCWQKERNHRPKFTDIVSFLDKLIRNPSALHTLVEDILVMPESPGEVPEY
PLFVTVGDWLDSIKMGQYKNNFVAAGFTTFDLISRMSIDDIRRIGVILIGHQRRIVSSIQ
TLRLHMMHIQEKGFHV

**Important features of the protein:**

**Signal peptide:**
Amino acids 1-22

**Transmembrane domain:**
Amino acids 551-571

**N-glycosylation sites:**
Amino acids 343-346;397-400;410-413;756-759

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 851-854

**Tyrosine kinase phosphorylation sites:**
Amino acids 483-490;604-612;787-794

**N-myristoylation sites:**
Amino acids 192-197;274-279;289-294;373-378;394-399;504-509;
757-762;777-782;781-786;900-905;976-981

**Amidation site:**
Amino acids 358-361;653-656

**Tyrosine protein kinases specific active-site signature:**
Amino acids 794-806

**Receptor tyrosine kinase class V signature 1:**
Amino acids 192-208

**Ephrin receptor ligand binding domain:**
Amino acids 34-207

**pkinase Protein kinase domain:**
Amino acids 631-927

**Fibronectin type III domain:**
Amino acids 332-425;440-527

**SAM domain (Sterile alpha motif):**
Amino acids 959-1023

# FIGURE 105

GGCGGCGGGCTGCGCGGAGCGGCGTCCCCTGCAGCCGCGGACCGAGGCAGCGGCGGCACCTGCCGGCCGAGCAA
TGCCAAGTGAGTACACCTATGTGAAACTGAGAAGTGATTGCTCGAGGCCTTCCCTGCAATGGTACACCCGAGCT
CAAAGCAAGATGAGAAGGCCCAGCTTGTTATTAAAAGACATCCTCAAATGTACATTGCTTGTGTTTGGAGTGTG
GATCCTTTATATCCTCAAGTTAAATTATACTACTGAAGAATGTGACATGAAAAAAATGCATTATGTGGACCCTG
ACCATGTAAAGAGAGCTCAGAAATATGCTCAGCAAGTCTTGCAGAAGGAATGTCGTCCCAAGTTTGCCAAGACA
TCAATGGCGCTGTTATTTGAGCACAGGTATAGCGTGGACTTACTCCCTTTTGTGCAGAAGGCCCCCAAAGACAG
TGAAGCTGAGTCCAAGTACGATCCTCCTTTTGGGTTCCGGAAGTTCTCCAGTAAAGTCCAGACCCTCTTGGAAC
TCTTGCCAGAGCACGACCTCCCTGAACACTTGAAAGCCAAGACCTGTCGGCGCTGTGTGGTTATTGGAAGCGGA
GGAATACTGCACGGATTAGAACTGGGCCACACCCTGAACCAGTTCGATGTTGTGATAAGGTTAAACAGTGCACC
AGTTGAGGGATATTCAGAACATGTTGGAAATAAAACTACTATAAGGATGACTTATCCAGAGGGCGCACCACTGT
CTGACCTTGAATATTATTCCAATGACTTATTTGTTGCTGTTTTATTTAAGAGTGTTGATTTCAACTGGCTTCAA
GCAATGGTAAAAAAGGAAACCCTGCCATTCTGGGTACGACTCTTCTTTTGGAAGCAGGTGGCAGAAAAAATCCC
ACTGCAGCCAAAACATTTCAGGATTTTGAATCCAGTTATCATCAAAGAGACTGCCTTTGACATCCTTCAGTACT
CAGAGCCTCAGTCAAGGTTCTGGGGCCGAGATAAGAACGTCCCCACAATCGGTGTCATTGCCGTTGTCTTAGCC
ACACATCTGTGCGATGAAGTCAGTTTGGCGGGTTTTGGATATGACCTCAATCAACCCAGAACACCTTTGCACTA
CTTCGACAGTCAATGCATGGCTGCTATGAACTTTCAGACCATGCATAATGTGACAACGGAAACCAAGTTCCTCT
TAAAGCTGGTCAAAGAGGGAGTGGTGAAAGATCTCAGTGGAGGCATTGATCGTGAATTTTGAACACAGAAAACC
TCAGTTGAAAATGCAACTCTAACTCTGAGAGCTGTTTTTGACAGCCTTCTTGATGTATTTCTCCATCCTGCAGA
TACTTTGAAGTGCAGCTCATGTTTTTAACTTTTAATTTAAAAACACAAAAAAAATTTTAGCTCTTCCCACTTTT
TTTTTCCTATTTATTTGAGGTCAGTGTTTGTTTTTGCACACCATTTTGTAAATGAAACTTAAGAATTGAATTGG
AAAGACTTCTCAAAGAGAATTGTATGTAACGATGTTGTATTGATTTTTAAGAAAGTAATTTAATTTGTAAAACT
TCTGCTCGTTTACACTGCACATTGAATACAGGTAACTAATTGGAAGGAGAGGGGAGGTCACTCTTTTGATGGTG
GCCCTGAACCTCATTCTGGTTCCCTGCTGCGCTGCTTGGTGTGACCCACGGAGGATCCACTCCCAGGATGACGT
GCTCCGTAGCTCTGCTGCTGATACTGGGTCTGCGATGCAGCGGCGTGAGGCCTGGGCTGGTTGGAGAAGGTCAC
AACCCTTCTCTGTTGGTCTGCCTTCTGCTGAAAGACTCGAGAACCAACCAGGGAAGCTGTCCTGGAGGTCCCTG
GTCGGAGAGGGACATAGAATCTGTGACCTCTGACAACTGTGAAGCCACCCTGGGCTACAGAAACCACAGTCTTC
CCAGCAATTATTACAATTCTTGAATTCCTTGGGGATTTTTTACTGCCCTTTCAAAGCACTTAAGTGTTAGATCT
AACGTGTTCCAGTGTCTGTCTGAGGTGACTTAAAAAATCAGAACAAAACTTCTATTATCCAGAGTCATGGGAGA
GTACACCCTTTCCAGGAATAATGTTTTGGGAAACACTGAAATGAAATCTTCCCAGTATTATAAATTGTGTATTTAA

# FIGURE 106

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA96897
><subunit 1 of 1, 362 aa, 1 stop
><MW: 41736, pI: 8.80, NX(S/T): 3
MRRPSLLLKDILKCTLLVFGVWILYILKLNYTTEECDMKKMHYVDPDHVKRAQKYAQQVLQK
ECRPKFAKTSMALLFEHRYSVDLLPFVQKAPKDSEAESKYDPPFGFRKFSSKVQTLLELLPE
HDLPEHLKAKTCRRCVVIGSGGILHGLELGHTLNQFDVVIRLNSAPVEGYSEHVGNKTTIRM
TYPEGAPLSDLEYYSNDLFVAVLFKSVDFNWLQAMVKKETLPFWVRLFFWKQVAEKIPLQPK
HFRILNPVIIKETAFDILQYSEPQSRFWGRDKNVPTIGVIAVVLATHLCDEVSLAGFGYDLN
QPRTPLHYFDSQCMAAMNFQTMHNVTTETKFLLKLVKEGVVKDLSGGIDREF

**Important features of the protein:**

**Transmembrane domain:**
Amino acids 11-27;281-297

**N-glycosylation sites:**
Amino acids 30-34;180-184;334-338

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 2-6;109-113;223-227

**N-myristoylation sites:**
Amino acids 146-152;150-156;179-185;191-197

# FIGURE 107

TGACGCGGGGCGCCAGCTGCCAACTTCGCGCGCGGAGCTCCCCGGCGGTGCAGTCCCGTCCCGGCGGCGCGG
GCGGCATGAAGACTAGCCGCCGCGGCCGAGCGCTCCTGGCCGTGGCCCTGAACCTGCTGGCGCTGCTGTTCG
CCACCACCGCTTTCCTCACCACGCACTGGTGCCAGGGCACGCAGCGGGTCCCCAAGCCGGGCTGCGGCCAGG
GCGGGCGCGCCAACTGCCCCAACTCGGGCGCCAACGCCACGGCCAACGGCACCGCCGCCCCCGCCGCCGCCG
CCGCCGCCGCCACCGCCTCGGGGAACGGCCCCCCTGGCGGCGCGCTCTACAGCTGGGAGACCGGCGACGACC
GCTTCCTCTTCAGGAATTTCCACACCGGCATCTGGTACTCGTGCGAGGAGGAGCTCAGCGGGCTTGGTGAAA
AATGTCGCAGCTTCATTGACCTGGCCCCGGCGTCGGAGAAAGGCCTCCTGGGAATGGTCGCCCACATGATGT
ACACGCAGGTGTTCCAGGTCACCGTGAGCCTCGGTCCTGAGGACTGGAGACCCCATTCCTGGGACTACGGGT
GGTCCTTCTGCCTGGCGTGGGGCTCCTTTACCTGCTGCATGGCAGCCTCTGTCACCACGCTCAACTCCTACA
CCAAGACGGTCATTGAGTTCCGGCACAAGCGCAAGGTCTTTGAGCAGGGCTACCGGGAAGAGCCGACCTTCA
TAGACCCTGAGGCCATCAAGTACTTCCGGGAGAGGATGGAGAAGAGGGACGGGAGCGAGGAGGACTTTCACT
TAGACTGCCGCCACGAGAGATACCCTGCCCGACACCAGCCACACATGGCGGATTCCTGGCCCCGGAGCTCCG
CACAGGAAGCACCAGAGCTGAACCGACAGTGCTGGGTCTTGGGGCACTGGGTGTGACCAAGACCTCAACCTG
GCCCGCGGACCTCAGGCCATCGCTGGCACCAGCCCCTGCTGCAAGACCACCAGAGTGGTGCCCCCAGAACCC
TGGCCTGTGTGCCGTGAACTCAGTCAGCCTGCGTGGGAGATGCCAGGCCTGTCCTGCCCATCGCTGCCTGGG
TCCCATGGCCTTGGAAATGGGGCCAGGGCAGGCCCAAGGGAATGCACAGGGCTGCACAGAGTGACTTTGGGA
CAGCAGCCCCGGACTCTTGCCATCATCACATGAGCCCTGCTGGGCACAGCTGCGATGCCAGGAGACACATGG
CCACTGGCCACTGAATGGCTGGCACCCACAAGCCAGTCAGGTGCCCAGAGGGGCAGAGCCCTTTGGGGGGCA
GAGAGTGGCTTCCTGAAGGAGGGGGCAGTGGCGCAGGCACTGCAGGGGTGTCACACAGCAGGCACACAGCAG
GGGCTCAATAAATGCTTGTTGAACTTGTTTT

# FIGURE 108

MKTSRRGRALLAVALNLLALLFATTAFLTTHWCQGTQRVPKPGCGQGGRANCPNSGANATANGTAAPAAAA
AAATASGNGPPGGALYSWETGDDRFLFRNFHTGIWYSCEEELSGLGEKCRSFIDLAPASEKGLLGMVAHMM
YTQVFQVTVSLGPEDWRPHSWDYGWSFCLAWGSFTCCMAASVTTLNSYTKTVIEFRHKRKVFEQGYREEPT
FIDPEAIKYFRERMEKRDGSEEDFHLDCRHERYPARHQPHMADSWPRSSAQEAPELNRQCWVLGHWV

Important features of the protein:

Signal peptide:
1-26

Transmembrane domain:
169-189

N-glycosylation site.
58-61
62-65

Glycosaminoglycan attachment site.
77-80
114-117

Tyrosine kinase phosphorylation site.
202-208

N-myristoylation site.
43-48
47-52
56-61
84-89
104-109
174-179

# FIGURE 109

GATTACCAAGCAAGAACAGCTAAA**ATG**AAAGCCATCATTCATCTTACTCTTCTTGCTCTCCT
TTCTGTAAACACAGCCACCAACCAAGGCAACTCAGCTGATGCTGTAACAACCACAGAAACTG
CGACTAGTGGTCCTACAGTAGCTGCAGCTGATACCACTGAAACTAATTTCCCTGAAACTGCT
AGCACCACAGCAAATACACCTTCTTTCCCAACAGCTACTTCACCTGCTCCCCCCATAATTAG
TACACATAGTTCCTCCACAATTCCTACACCTGCTCCCCCCATAATTAGTACACATAGTTCCT
CCACAATTCCTATACCTACTGCTGCAGACAGTGAGTCAACCACAAATGTAAATTCATTAGCT
ACCTCTGACATAATCACCGCTTCATCTCCAAATGATGGATTAATCACAATGGTTCCTTCTGA
AACACAAAGTAACAATGAAATGTCCCCCACCACAGAAGACAATCAATCATCAGGGCCTCCCA
CTGGCACCGCTTTATTGGAGACCAGCACCCTAAACAGCACAGGTCCCAGCAATCCTTGCCAA
GATGATCCCTGTGCAGATAATTCGTTATGTGTTAAGCTGCATAATACAAGTTTTTGCCTGTG
TTTAGAAGGGTATTACTACAACTCTTCTACATGTAAGAAAGGAAAGGTATTCCCTGGGAAGATT
TCAGTGACAGTATCAGAAACATTTGACCCAGAAGAGAAACATTCCATGGCCTATCAAGACTT
GCATAGTGAAATTACTAGCTTGTTTAAAGATGTATTTGGCACATCTGTTTATGGACAGACTG
TAATTCTTACTGTAAGCACATCTCTGTCACCAAGATCTGAAATGCGTGCTGATGACAAGTTT
GTTAATGTAACAATAGTAACAATTTTGGCAGAAACCACAAGTGACAATGAGAAGACTGTGAC
TGAGAAAATTAATAAAGCAATTAGAAGTAGCTCAAGCAACTTTCTAAACTATGATTTGACCC
TTCGGTGTGATTATTATGGCTGTAACCAGACTGCGGATGACTGCCTCAATGGTTTAGCATGC
GATTGCAAATCTGACCTGCAAAGGCCTAACCCACAGAGCCCTTTCTGCGTTGCTTCCAGTCT
CAAGTGTCCTGATGCCTGCAACGCACAGCACAAGCAATGCTTAATAAAGAAGAGTGGTGGGG
CCCCTGAGTGTGCGTGCGTGCCCGGCTACCAGGAAGATGCTAATGGGAACTGCCAAAAGTGT
GCATTTGGCTACAGTGGACTCGACTGTAAGGACAAATTTCAGCTGATCCTCACTATTGTGGG
CACCATCGCTGGCATTGTCATTCTCAGCATGATAATTGCATTGATTGTCACAGCAAGATCAA
ATAACAAAACGAAGCATATTGAAGAAGAGAACTTGATTGACGAAGACTTTCAAAATCTAAAA
CTGCGGTCGACAGGCTTCACCAATCTTGGAGCAGAAGGGAGCGTCTTTCCTAAGGTCAGGAT
AACGGCCTCCAGAGACAGCCAGATGCAAAATCCCTATTCAAGCCACAGCAGCATGCCCCGCC
CTGACTAT**TAG**AATCATAAGAATGTGGAACCCGCCATGGCCCCCAACCAATGTACAAGCTAT
TATTTAGAGTGTTTAGAAAGACTGATGGAGAAGTGAGCACCAGTAAAGATCTGGCCTCCGGG
GTTTTTCTTCCATCTGACATCTGCCAGCCTCTCTGAATGGAAGTTGTGAATGTTTGCAACGA
ATCCAGCTCACTTGCTAAATAAGAATCTATGACATTAAATGTAGTAGATGCTATTAGCGCTT
GTCAGAGAGGTGGTTTTCTTCAATCAGTACAAAGTACTGAGACAATGGTTAGGGTTGTTTTC
TTAATTCTTTTCCTGGTAGGGCAACAAGAACCATTTCCAATCTAGAGGAAAGCTCCCCAGCA
TTGCTTGCTCCTGGGCAAACATTGCTCTTGAGTTAAGTGACCTAATTCCCCTGGGAGACATA
CGCATCAACTGTGGAGGTCCGAGGGGATGAGAAGGGATACCCACCATCTTTCAAGGGTCACA
AGCTCACTCTCTGACAAGTCAGAATAGGGACACTGCTTCTATCCCTCCAATGGAGAGATTCT
GGCAACCTTTGAACAGCCCAGAGCTTGCAACCTAGCCTCACCCAAGAAGACTGGAAAGAGAC
ATATCTCTCAGCTTTTTCAGGAGGCGTGCCTGGGAATCCAGGAACTTTTTGATGCTAATTAG
AAGGCCTGGACTAAAAATGTCCACTATGGGGTGCACTCTACAGTTTTTGAAATGCTAGGAGG
CAGAAGGGGCAGAGAGTAAAAAACATGACCTGGTAGAAGGAAGAGAGGCAAAGGAAACTGGG
TGGGGAGGATCAATTAGAGAGGAGGCACCTGGGATCCACCTTCTTCCTTAGGTCCCCTCCTC
CATCAGCAAAGGAGCACTTCTCTAATCATGCCCTCCCGAAGACTGGCTGGGAGAAGGTTTAAAA
ACAAAAAATCCAGGAGTAAGAGCCTTAGGTCAGTTTGAAATTGGAGACAAACTGTCTGGCAA
AGGGTGCGAGAGGGAGCTTGTGCTCAGGAGTCCAGCCGCCCAGCCTCGGGGTGTAGGTTTCT
GAGGTGTGCCATTGGGGCCTCAGCCTTCTCTGGTGACAGAGGCTCAGCTGTGGCCACCAACA
CACAACCACACACACACAACCACACACACAAATGGGGGCAACCACATCCAGTACAAGCTTTT
ACAAATGTTATTAGTGTCCTTTTTTATTTCTAATGCCTTGTCCTCTTAAAAGTTATTTTATT
TGTTATTATTATTTGTTCTTGACTGTTAATTGTGAATGGTAATGCAATAAAGTGCCTTTGTT
AGATGGTGAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

# FIGURE 110

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA142930
><subunit 1 of 1, 512 aa, 1 stop
><MW: 54535, pI: 4.89, NX(S/T): 7
MKAIIHLTLLALLSVNTATNQGNSADAVTTTETATSGPTVAAADTTETNFPETASTTANT
PSFPTATSPAPPIISTHSSSTIPTPAPPIISTHSSSTIPIPTAADSESTTNVNSLATSDI
ITASSPNDGLITMVPSETQSNNEMSPTTEDNQSSGPPTGTALLETSTLNSTGPSNPCQDD
PCADNSLCVKLHNTSFCLCLEGYYYNSSTCKKGKVFPGKISVTVSETFDPEEKHSMAYQD
LHSEITSLFKDVFGTSVYGQTVILTVSTSLSPRSEMRADDKFVNVTIVTILAETTSDNEK
TVTEKINKAIRSSSSNFLNYDLTLRCDYYGCNQTADDCLNGLACDCKSDLQRPNPQSPFC
VASSLKCPDACNAQHKQCLIKKSGGAPECACVPGYQEDANGNCQKCAFGYSGLDCKDKFQ
LILTIVGTIAGIVILSMIIALIVTARSNNKTKHIEEENLIDEDFQNLKLRSTGFTNLGAE
GSVFPKVRITASRDSQMQNPYSSHSSMPRPDY

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-17

**Transmembrane domain:**
Amino acids 421-442

**N-glycosylation sites:**
Amino acids 151-155;169-173;193-197;206-210;284-288;
332-336;449-453

**N-myristoylation sites:**
Amino acids 330-336;385-391;427-433;478-484

**SEA domain:**
Amino acids 212-328

# FIGURE 111

CTGGGACTTGGCTTTCTCCGGATAAGCGGCGGCACCGGCGTCAGCG**ATG**ACCGTGCAGAGAC
TCGTGGCCGCGGCCGTGCTGGTGGCCCTGGTCTCACTCATCCTCAACAACGTGGCGGCCTTC
ACCTCCAACTGGGTGTGCCAGACGCTGGAGGATGGGCGCAGGCGCAGCGTGGGGCTGTGGAG
GTCCTGCTGGCTGGTGGACAGGACCCGGGGAGGGCCGAGCCCTGGGGCCAGAGCCGGCCAGG
TGGACGCACATGACTGTGAGGCGCTGGGCTGGGGCTCCGAGGCAGCCGGCTTCCAGGAGTCC
CGAGGCACCGTCAAACTGCAGTTCGACATGATGCGCGCCTGCAACCTGGTGGCCACGGCCGC
GCTCACCGCAGGCCAGCTCACCTTCCTCCTGGGGCTGGTGGGCCTGCCCCTGCTGTCACCCG
ACGCCCCGTGCTGGGAGGAGGCCATGGCCGCTGCATTCCAACTGGCGAGTTTTGTCCTGGTC
ATCGGGCTCGTGACTTTCTACAGAATTGGCCCATACACCAACCTGTCCTGGTCCTGCTACCT
GAACATTGGCGCCTGCCTTCTGGCCACGCTGGCGGCAGCCATGCTCATCTGGAACATTCTCC
ACAAGAGGGAGGACTGCATGGCCCCCCGGGTGATTGTCATCAGCCGCTCCCTGACAGCGCGC
TTTCGCCGTGGGCTGGACAATGACTACGTGGAGTCACCATGC**TGA**GTCGCCCTTCTCAGCGC
TCCATCAACGCACACCTGCTATCGTGGAACAGCCTAGAAACCAAGGGACTCCACCACCAAGT
CACTTCCCCTGCTCGTGCAGAGGCACGGGATGAGTCTGGGTGACCTCTGCGCCATGCGTGCG
AGACACGTGTGCGTTTACTGTTATGTCGGTCATATGTCTGTACGTGTCGTGGGCCAACCTCG
TTCTGCCTCCAGC

# FIGURE 112

>></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA147253
><subunit 1 of 1, 226 aa, 1 stop
><MW: 24540, pI: 8.27, NX(S/T): 1
MTVQRLVAAAVLVALVSLILNNVAAFTSNWVCQTLEDGRRRSVGLWRSCWLVDRTRGGPS
PGARAGQVDAHDCEALGWGSEAAGFQESRGTVKLQFDMMRACNLVATAALTAGQLTFLLG
LVGLPLLSPDAPCWEEAMAAAFQLASFVLVIGLVTFYRIGPYTNLSWSCYLNIGACLLAT
LAAAMLIWNILHKREDCMAPRVIVISRSLTARFRRGLDNDYVESPC

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-25

**Transmembrane domains:**
Amino acids 105-125;139-157;169-188

**N-glycosylation site:**
Amino acids 164-168

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**
Amino acids 39-43

**Tyrosine kinase phosphorylation site:**
Amino acids 214-222

**N-myristoylation sites:**
Amino acids 44-50;62-68;66-72;79-85

**Amidation site:**
Amino acids 37-41

# FIGURE 113

GACTTTACCACTACTCGCTATAGAGCCCTGGTCAAGTTCTCTCCACCTCTCTATCTATGTCT
CAGTTTCTTCATCTGTAACATCAAATGAATAATAATACCAATCTCCTAGACTTCATAAGAGG
ATTAACAAAGACAAAATATGGGAAAAACATAACATGGCGTCCCATAATTATTAGATCTTATT
ATTGACACTAAAATGGCATTAAAATTACCAAAAGGAAGACAGCATCTGTTTCCTCTTTGGTC
CTGAGCTGGTTAAAAGGAACACTGGTTGCCTGAACAGTCACACTTGCAACC**ATG**ATGCCTAA
ACATTGCTTTCTAGGCTTCCTCATCAGTTTCTTCCTTACTGGTGTAGCAGGAACTCAGTCAA
CGCATGAGTCTCTGAAGCCTCAGAGGGTACAATTTCAGTCCCGAAATTTTCACAACATTTTG
CAATGGCAGCCTGGGAGGGCACTTACTGGCAACAGCAGTGTCTATTTTGTGCAGTACAAAAT
ATATGGACAGAGACAATGGAAAAATAAAGAAGACTGTTGGGGTACTCAAGAACTCTCTTGTG
ACCTTACCAGTGAAACCTCAGACATACAGGAACCTTATTACGGGAGGGTGAGGGCGGCCTCG
GCTGGGAGCTACTCAGAATGGAGCATGACGCCGCGGTTCACTCCCTGGTGGGAAACAAAAAT
AGATCCTCCAGTCATGAATATAACCCAAGTCAATGGCTCTTTGTTGGTAATTCTCCATGCTC
CAAATTTACCATATAGATACCAAAAGGAAAAAAATGTATCTATAGAAGATTACTATGAACTA
CTATACCGAGTTTTTATAATTAACAATTCACTAGAAAAGGAGCAAAAGGTTTATGAAGGGGC
TCACAGAGCGGTTGAAATTGAAGCTCTAACACCACACTCCAGCTACTGTGTAGTGGCTGAAA
TATATCAGCCCATGTTAGACAGAAGAAGTCAGAGAAGTGAAGAGAGATGTGTGGAAATTCCA
**TGA**CTTGTGGAATTTGGCATTCAGCAATGTGGAAATTCTAAAGCTCCCTGAGAACAGGATGA
CTCGTGTTTGAAGGATCTTATTTAAAATTGTTTTTGTATTTTCTTAAAGCAATATTCACTGT
TACACCTTGGGGACTTCTTTGTTTACCCATTCTTTTATCCTTTATATTTCATTTGTAAACTA
TATTTGAACGACATTCCCCCCGAAAAATTGAAATGTAAAGATGAGGCAGAGAATAAAGTGTT
CTATGAAATTCAGAACTTTATTTCTGAATGTAACATCCCTAATAACAACCTTCATTCTTCTA
ATACAGCAAAATAAAAATTTAACAACCAAGGAATAGTATTTAAGAAAATGTTGAAATAATTT
TTTTAAAATAGCATTACAGACTGAG

# FIGURE 114

></usr/seqdb2/sst/DNA/Dnaseqs.min/ss.DNA149927
><subunit 1 of 1, 231 aa, 1 stop
><MW: 26980, pI: 7.06, NX(S/T): 5
MMPKHCFLGFLISFFLTGVAGTQSTHESLKPQRVQFQSRNFHNILQWQPGRALTGNSSVY
FVQYKIYGQRQWKNKEDCWGTQELSCDLTSETSDIQEPYYGRVRAASAGSYSEWSMTPRF
TPWWETKIDPPVMNITQVNGSLLVILHAPNLPYRYQKEKNVSIEDYYELLYRVFIINNSL
EKEQKVYEGAHRAVEIEALTPHSSYCVVAEIYQPMLDRRSQRSEERCVEIP

**Important features of the protein:**
**Signal peptide:**
Amino acids 1-21

**N-glycosylation sites:**
Amino acids 56-60;134-138;139-143;160-164;177-181

**N-myristoylation sites:**
Amino acids 18-24;21-27;189-195